

FIGURE 1

CCAGGTCCA ACTGCACCTCGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACCGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCCAGTGGCCTGAGGCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGCCACGCCGGC
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCACCACCCGGAGG
AGCAGCTCCTGCCCTGTCCGGGG**ATG**ACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGA
AGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGCTCTCAGGAGGTGCTGCTGATGTGGCT
TCTGGTGGTGGCAGTGGCGGACAGAGCACGCCTACCGGCCGGCCGTTAGGGTGTGCT
GTCCCAGGCTCACGGGACCCCTGTCTCCGAGTCGTTCGTGCAGCGTGTGACCAGCCCTCC
TCACCACCTGCGACGGGACCGGCCCTGCAGCACCTACCGAACCATTTATAGGACCGCCTAC
CGCCGAGCCCTGGCTGCCAGGCCTCGCTACCGTGCTGCCGGCTGGAAGAG
GACCAGCGGGCTTCCTGGGCCTGTGGAGCAGCAATATGCCAGGCCATGCCGGAACGGAG
GGAGCTGTGTCCAGCCTGGCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCAG
TCAGATGTGGATGAATGCAGTGCTAGGAGGGCGGCTGTCCCCAGCGCTGCATCACACCGC
CGGCAGTTACTGGTGCCAGTGGTGGAGGGGACAGCCTGTGAGACGGTACACTCTGTG
TGCCCAAGGGAGGGCCCCCAGGGTGGCCCCAACCCGACAGGAGTGGACAGTGCAATGAAG
GAAGAAGTGCAGAGGCTGCAGTCAGGGTGGACCTGCTGGAGGAGAACGCTGCAGCTGGT
GGCCCCACTGCACAGCCTGGCCTCGCAGGCAGTGGAGCATGGCTCCGGACCCGGCAGCC
TCCTGGTGCACTCCTCCAGCAGCTGGCCGATCGACTCCCTGAGCGAGCAGATTCCTTC
CTGGAGGAGCAGCTGGGTCTGCTCCTGCAAGAAAGACTCGT**G**ACTGCCAGCGCCCCAGG
CTGGACTGAGCCCTCACGCCGCCCTGCAGCCCCATGCCCTGCCAACATGCTGGGGTC
CAGAACCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCTTCCTCCTTTCTCCTC
CCCTCCCTCGGGAGGGTCCCCAGACCCCTGGCATGGATGGCTGGATTTTTGTGAAT
CCACCCCTGGCTACCCCCACCCCTGGTTACCCCAACGGCATCCAAAGGCCAGGTGGCCCTCA
GCTGAGGGAAGGTACGAGTTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCC
CGGAGGCTGGTGGGCCTCAGTGGGGCTGCTGCCGTACCCCCAGCACAATAAAATGAAA
CGTGAaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaAGGGCGGCCGCACTCT
AGAGTCGACCTGCAGAACGCTGGCCGCATGCCCAACTTGTGTTATTGCAGCTTATAATGGT
TACAAAT

FIGURE 2

MTDSPPPGHPEEKATPPGGTGHEGLSGGAADVASGVGSGRHRARLPARPLGCVLSRAHDPV
SESFVQRVYQPFLTTCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGAC
GAAICQPPCRNGGSCVQPGRCRCPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCW
EGHSLSADGTLCPKGGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLAS
QALEHGLPDPGSLLVHSFQQQLGRIDLSEQISFLEEQLGSCSCKKDS

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 93-97, 270-274

N-myristoylation sites.

amino acids 19-25, 78-84, 97-103, 100-106, 103-109, 157-163,
191-197, 265-271

Amidation site.

amino acids 26-30

Aspartic acid and asparagine hydroxylation site.

amino acids 152-164

Cell attachment sequence.

amino acids 130-133

EGF-like domain cysteine pattern signature.

amino acids 123-135

FIGURE 3

CGCTCGCCCCGTCGCCCTGCCCTCCCCCAGAGTCAGCTCGCGGAGCAGATGTGTGGG
GTCAGCCCACGGCGGGACTATGGTGAATTCCCGCGCTACGCACTACTGGCCCTGATC
CGGTTCTTGGTGCCTGGCATACCAACATAGCCATCGACTTCGGGAGCAGGCCCTGAA
CGGGGCATTGCTGCTCAAGGAGGATGCAGTCGAGATGCTGCCAGCTACGGGCTGGCGT
ACTCCCTCATGAAGTTCTCACGGGTCCTAGAGTGAACCTCAAAATGTGGGCTGGTGT
GTGAACAGCAAGAGAGACAGGACAAAGCCGTCTGTATGGTGGTGGCAGGGCCATCGC
TGCCGTCTTCACACACTGATAGCTTATAGTGAATTAGGATACTACATTATCAATAAACTGC
ACCATGTGGACGGAGTCGGTGGGAGCAAGACGAGAAGGGCTTCTGTACCTCGCCCTT
CCTTCATGGACGCAATGGCATGGACCCATGCTGGCATTCTCTTAAACACAAATACAGTT
CCTGGTGGATGTGCCTCAATCTCAGATGTCAAGCTCAGGTTGTTTAGCCATTGTC
TTCACAGTCACCTGGAATGCCGGAGGCCCTGCTCATCCGATCCTCTCCTGTACATGGC
GCACTTGTGCCTGCACCACCCCTGTGCCTGGCTACTACAAGAACATTACGACATCATCCC
TGACAGAAGTGGCCGGAGCTGGGGAGATGCAACAATAAGAAAGATGCTGAGCTCTGGT
GGCCTTGGCTTAATTCTGCCACACAGAGAATCAGTCGGCCTATTGTCAACCTCTTGT
TCCCAGGACCTGGTGGCAGTTCTGCAGCCACAGAGGAGTGGCATTGACAGCCACATA
CCCTGTGGGTACATGCCATACGGCTGGTGACGGAAATCCGTGCTGTATCCTGCTTCG
ACAAGAATAACCCAGCAACAAACTGGTGAGCACGAGCAACACAGTCACGGCAGGCCACATC
AAGAAGTTCACCTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTCTGTGATGTTGGAC
ACCCACGTGCTGAGAAAATCTGATAGACATCATCGGAGTGGACTTGCCTTGCAGAAC
TCTGTGTTGTTCTTGCAGTCTCCTTCTCCAGTTCCAGTCACAGTGAGGGCGCAT
CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTCCTGCCCTCAGCTCTGCTGCG
GATCATCGTCCTCATGCCAGCCTCGTGGCTACCTCACGAGGGTGACGGTGCACGGCAGCC
TGGCGTGGCTCCCTCTGGCGGGCTTGTGGGAGAATCCACCATGGTCGCCATCGTGC
TGCTATGTCTACCGGAAGCAGAAAAGAAGATGGAGAATGAGTCGGCCACGGAGGGGAAGA
CTCTGCCATGACAGACATGCCCTCGACAGAGGAGGTGACAGACATCGTGGAAATGAGAGAGG
AGAATGAATAAGGCACGGACGCCATGGCACTGCAGGGACGGTCACTCAGGATGACACTTC
GGCATCATCTCCCTCTCCATCGTATTTGTTCCCTTTTTGTTGTTGGTAAT
GAAAGAGGCCTGATTAAAGGTTCTGTCATTCTCTAGCATACTGGGTATGCTCACACT
GACGGGGGGACCTAGTGAATGGTCTTACTGTTGCTATGAAAAACAAACGAAACAATGAC
TTCATACCCCTGCCTCACGAAACCCAAAAGACACAGTCGCTCACGGTTGACGTTGTC
TCCTCCCTGGACAATCCTCTGGAACCAAGGACTGCAGCTGCCATCGCCTCGGT
CACCTGCACAGCAGGCCACAGACTCTCCTGTCCTCCATCGCTCTTAAGAATCAACAGG
TTAAAACCTGGCTCCTTGATTGCTTCCAGTCACATGGCGTACAAAGAGATGGAGGCC
CGGTGGCCTCTAAATTCCCTCTGCCACGGAGTTGAAACCATCTACTCCACACATGCAG
GAGGCGGGTGGCACGCTGCAGCCGGAGTCCCCTTCACACTGAGGAACGGAGACCTGTGAC
CACAGCAGGCTGACAGATGGACAGAAATCTCCGTAGAAAGGTTGGTTGAAATGCCCGGG
GGCAGCAAACGTGACATGGTGAATGATAGCATTCACTCTGCTTCTCTAGATCTGAGCAA
GCTGTCAGTCTCACCCCCACCGTGTATATACATGAGCTAACCTTTAAATTGTCAACAAA
GCGCATCTCCAGATTCCAGACCCCTGCCCATGACTTTCTGAAAGGCTGCTTCCCTCGC
CTTCCCTGAAGGTCGATTAGAGCGAGTCACATGGAGCATCCTAACCTTGCACTTGT
TACAGTGAACTGAAGCTTAAGTCTCATCCAGCATTCTAATGCCAGGTTGCTGTAGGGTAAC
TTTGAAGTAGATATATTACCTGGTTCTGCTATCCTTAGTCATACTCTGCGGTACAGGTA
TTGAGAATGTACTACGGTACTTCCCTCCACACCATAACGATAAAGCAAGACATTATAACG
ATACCAAGAGTCACTATGTGGTCCTCCCTGAAATAACGCAATTGAAATCCATGCACTGAGTA
TATTTTCTAAGTTGGAAAGCAGGTTTTCTTAAACAAATATAGACACGGTTCACT
AAATTGATTAGTCAGAATTCTAGACTGAAAGAACCTAAACAAAAAAATATTTAAAGATA
TAAATATATGCTGTATATGTTATGTAATTATTTAGGCTATAATACATTCCATTTCG
ATTTCATAAAATGTCTCTAATACAAAAAA

FIGURE 4

MVKFPALTHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMKFF
TGPMMSDFKNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYIINKLHHVDESV
GSKTRRAFLYLAAPFMDAMAWTAGILLKHKSFLVGCAISDVIAQVVFVAILLHSHLEC
REPLLIPILSLYMGALVRCTTLCGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLALIL
ATQRISRPIVNLFVSRLGGSSAATEAVAILTATYPVGHMPYWLTEIRAVYPAFDKNNPSN
KLVSTSNTVTAAHIKKFTFVCMALSLTLCFVMFWTPNVSEKILIDIIGVDFAFELCVVPLR
IFSFFPVPVTVRAHTGWLMTLKKTFLAPSSVLRIIVLIAASLVVLPYLGVHGATLGVGSLL
AGFVGESTMVAIAACYVYRKOKKKMENESATEGEDSAMTDMPPTEEVTDIVEMREENE

Transmembrane domains:

amino acids 86-106, 163-179, 191-205, 237-253, 327-343, 357-374, 408-423, 431-445

FIGURE 5

CCTGACAGAAGTGC~~CCCCGGAGCTGGGGAGATNCAACATTAAGAAGATGCTGAGCTCTGGT~~
GCCNTTGGCTCTAATTCTGCCACACAGAGAANCAGTCGGCCTATTGTCAACCTCTTGTT
TCCC~~GGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTGACAGCCACATA~~
CCCTGTGGGT~~CACATGCCATACGGCTGGTGACGGAAATCCGTGCTGTATCCTGCTTCG~~
ACAAGAATAACCCCAGCAACAAACTGGTGAGCAGCAGAACACAGTCACGGCGGCCACATC
AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTCGT~~GATGTTGGAC~~
ACCCAACGTG~~TCTGNGAAAATCTGATAGACATCATGGAGTGGACTTGCCTTGACAAAC~~
TCTGTGTTGTT~~CTTGC~~GGATCTCCTTCTTCCAGTCAGTCACAGTGAGGGCGCAT
CTCACCGGGTGGCTGATGACACTGAAGAAAAC~~CTTCGTC~~

FIGURE 6

TGACGGAATCCGGGCTGGTATCCTGGTTNGACAAGATAAACCCCCAGCAANAAATTGGG
GAGCAGGGCAAAACAGTNACGGGCAGCCCACATCAAGAAGTTCACCTNGTTGNATGGNTCT
TGTCAACTCACGCTNTGTTCGTGTGATGTTGGACACCCAAAGTGGTGGAGAAAATTGGAT
AGACATNATCGGAGTGGANTTGCCTTGAGAANTTGNNTGTTGCCTTGCGGATTTCT
CCTTTTCCCAGTCCAGTCACAGNGAGGGCGCATCTCACCGGGNGNTGATGACANTGAAG
AAAACCTTGTCCTGCCCGCAGCTNTTGGTGCAGATCATTGTCCTNATNGCCAGCCTTGT
GGTCCTACCTACCTGGGGTGCACGGTGCAGCCTGGCGTGGGTTCCCTCCTGGCGGGCA

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FIGURE 7

TATTCCCAGTCCGGTCACGGGAGGGCGATNTCACCGGGTGGCTGANGACACTGAAGAAA
ACCTTNGTCCTGCCCGCAGNTTGTGNTGCGGATNATCGTCCTCATGCCAGCCTNGTGGT
CCTACCCCTACCTGGGGTGCACGGTGAGAC

卷之三

FIGURE 8

CCCCCGCGCCGGCGCCGGCGCCGAAGCCGGAGCCACCGCCATGGGGCCTGCCTGGGA
GCCTGCTCCCTGCTCAGCTGCGCGTCCTGCCTCTGCGGCTCTGCCCGCTGCATCCTGTGCAG
CTGCTGCCCGCCAGCCGAACCTCCACCGTGAGCCGCCTCATCTTCACGTTCTCCTCTTCC
TGGGGGTGCTGGTGTCCATCATTATGCTGAGCCGGCGTGGAGAGTCAGCTCTACAAGCTG
CCCTGGGTGTGAGGAGGGGCCGGATCCCCACCGCCTGCAGGGCCACATGACTGTGG
CTCCCTGCTTGGCTACCGCGCTGTCTACCGCATGTGCTCGCCACGGCGGCCTCTTCTTCT
TCTTTTCAACCTGCTCATGCTCTGCGTGAGCAGCAGCCGGACCCCCGGCTGCCATCCAG
AATGGGTTTGGTTCTTAAGTTCTGATCCTGGTGGGCCTCACCGTGGTGCCTTACAT
CCCTGACGGCTCCTCACCAACATCTGGTCTACTTCGGCGTGTGGCTCCTCCTTCA
TCCTCATCCAGCTGGTGCTGCTCATCGACTTGCACACTCCTGGAACCAGCGGTGGCTGGC
AAGGCCGAGGAGTGCATTCCCGTGCCTGGTACGCAGGCCTCTTCTTCACTCTCCTCTT
CTACTTGCTGTCGATCGCGGCCGTGGCGCTGATGTTCATGTACTACACTGAGCCCAGCGGCT
GCCACGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTCTGTGTCTGCGTGTCCATCGCT
GCTGTCCTGCCCAAGGTCCAGGACGCCAGCCAACTCGGGTCTGCTGCAGGCCTCGGTCT
CACCCCTACACCATGTTGTCACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCA
ACCCCATTTGCCAACCCAGCTGGCAACGAGACAGTTGTGGCAGGCCCGAGGGCTATGAG
ACCCAGTGGTGGATGCCCGAGCATTGTGGCCTCATCATCTCCTCCTGTGCACCCCTTT
CATCAGTCTGCGCTCCTCAGACCACCGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCC
CACCTATGCTAGACGCCACACAGCAGCAGCAGCAGCAGGTGGCAGCCTGTGAGGGCCGGCC
TTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTCTTCAACTTGTGCCTGGTGT
GGCCTCACTGCACGTATGATGACGCTCACCAACTGGTACAAGCCCGTGAGACCCGGAAGA
TGATCAGCACGTGGACCGCCGTGTGGTGAAGATCTGTGCCAGCTGGCAGGGCTGCTCCTC
TACCTGTGGACCCCTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGCTGAAGGAGCCT
CACAGCCTGCCATCTGGTGCCTCCTGCCACCTGGTGCCTCTGGCTCGGTGACAGCCAACCT
GCCCTCCCCAACCAATCAGCCAGGCTGAGCCCCACCCCTGCCAGCTCCAGGACCTG
CCCCTGAGCCGGCCTCTAGTCGTAGTGCCTCAGGGTCCGAGGAGCATCAGGCTCCTGCA
GAGCCCCATCCCCCGCCACACCCACACGGTGGAGCTGCCTCTCCTCCCTCCCTGT
TGCCCATACTCAGCATCTGGATGAAAGGGCTCCCTGTCTCAGGCTCCACGGAGCGGG
CTGCTGGAGAGAGCGGGAACTCCCACACAGTGGGCATCCGGCACTGAAGCCCTGGTGT
CCTGGTCACGTCCCCCAGGGACCCCTGCCCTGGACTTCGTGCCTTACTGAGTCTCT
AAGACTTTTCTAATAACAAGCCAGTGCCTGTAAAAAAA

FIGURE 9

MGACLGACSLSCASCLCGSAPCILCSCCPASRNSTVSRLIFTFFLFLGVLVSIIMLSPGVE
SQLYKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFTLLMLCVSSRD
PRAAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGGSFLFILIQLVLLIDFAH
NQRWLGAEECDRSAWYAGLFFFLLFYLLSIAAVALMFYYTEPSGCHEGKVFISLNLTFC
VCVSIAAVLPKVQDAQPNSGLLQASVITLYTMFVTSALSSIPEQKCNPHLPTQLGNETVVA
GPEGYETQWWDAPSIVGLIIFLLCTLFISLRSSDHQRQVNSLMQTEECPPMLDATQQQQQQVA
ACEGRAFDNEQDGVTYSYSFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVWVKICAS
WAGLLLYLWTLVAPLLLNRDFS

Signal sequence:

amino acids 1-20

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

FIGURE 10

GAGCGAGGCCGGGACTGAAGGTGTGGTGTGAGCCCTGGCAGAGGTTAACCTGGTC
AAATGCACGGATTCTCACCTCGTACAGTTACGCTCTCCCGGGCACGTCCGCGAGGACTTGA
AGTCCTGAGCGCTCAAGTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGC
ACCGCGGAGCTTCTCTGTAGAGCATTGTGCCTATTCCCCGAGTCTTGCTGCCGAAGCTG
TGACTGCCGATTCGGAAGTCCTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCC
TATTACCGGAATCTGGATGGGACCGCCTCCGGAGCTGTTGGCAAAGATGAACAGCAGAG
AATTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGG
TGTATGGGAAATACCAAGCTTTATTGATGCTAAACAACAATACATTGAGCAGAGCCAGGCA
GAAATTATCATAACCGGTTGATGCTGTGCAATCTGCACATCGTGTGCCACACGAGGCTT
CATTGTTATGGCTGGCGCTGGGTTGGAGAACTGCAGTGTGACTATATTCAACACAG
TGAACACTAGTCTGAATGTATAACGAAATAAGATGCCTTAAGCCATTGTAATTGCAGGA
GCTGTCACGGGAAGTCTTTAGGATAAACGTTAGGCCTGCGTGGCCTGGCTGGCTGGCAT
AATTGGAGCCTGCTGGCACTCCTGTAGGAGGCCTGCTGATGGCATTTCAGAAAGTACGCTG
GTGAGACTGTTAGGAAAGAAAACAGAAGGATCGAAAGGCCTCCATGAGCTAAACTGGAA
GAGTGGAAAGGCAGACTACAAGTTACTGAGCACCTCCCTGAGAAATTGAAAGTAGTTACG
GGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAAGCACTGCTAAACCTCCTAGAAACC
CTTCAGTAATAGATAAACAGACAAGGACTGAAAGTGTCTGAAACTCACTGGAGA
GCTGAAGGGAGCTGCCATGTCCGATGAAATGCCAACAGACAGGCCACTTTGGTCAGCCTGC
TGACAAATTAAAGTGTGGTACCTGTGGCAGTGGCTTGCTCTGTCTTTCTTTCTT
TTTAACTAAGAATGGGCTGTTGACTCTCACTTACTTATCCTAAATTAAACATAACT
TATGTTGTATTAATCTATCAATATATGCATACATGGATATATCCACCCACCTAGATTTAA
GCAGTAAATAAACATTGCAAAAGATTAAGTGAATTACAGTTT

FIGURE 11

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318
><subunit 1 of 1, 285 aa, 1 stop
><MW: 32190, pI: 9.03, NX(S/T): 2
MEVPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRRLRELF
GKDEQQRISKDLANICKTAATAGIIGWVYGGIPAFIHKQQYIEQSQAEIYHNRFDAVQSAH
RAATRGFIRYGWRWGWRGRTAVFVTIFNTVNTSLNVYRNKDALSHFVIAGAVTGSFRINVGLR
GLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDRKALHELKLEEWKGRLQVTEHLPE
KIESSLREDEPENDAKKIEALLNLPRNPSVIDKQDKD
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Important Features:

Signal Peptide:

amino acids 1-24

Transmembrane domains:

amino acids 76-96 and 171-195

N-glycosylation site:

amino acids 153-156

FIGURE 12

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATCTGGATGGGACCGCTCCGGAGCTGTTGGCAAAGATGAACAGCAGAGAATTCAAAGGA
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGAA
TACCAGCTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTATCAT
AACCGGTTTGTGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTGTTCATG
GCTGGCGCCGAACC

FIGURE 13

TCAAGTTGTCCGTAGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGGAGCTT
TTTCTGTAGAGCATTGTGCCTATTCCCCGAGTTTGCTGCCGAAGCTGTGACTGCCGAT
TCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCGGA
ATTTGGATGGGACCGCCTCCGGAGCTGTTGGCAAAGATGAACAGCAGAGAATTCAAAGG
ACCTTGCTGATATNTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGA
ATACCAGCTTTATTCATGNTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTATNA
TAACC

2000 1999 1998 1997 1996 1995 1994 1993 1992 1991 1990 1989 1988 1987 1986 1985 1984 1983 1982 1981 1980 1979 1978 1977 1976 1975 1974 1973 1972 1971 1970 1969 1968 1967 1966 1965 1964 1963 1962 1961 1960 1959 1958 1957 1956 1955 1954 1953 1952 1951 1950 1949 1948 1947 1946 1945 1944 1943 1942 1941 1940 1939 1938 1937 1936 1935 1934 1933 1932 1931 1930 1929 1928 1927 1926 1925 1924 1923 1922 1921 1920 1919 1918 1917 1916 1915 1914 1913 1912 1911 1910 1909 1908 1907 1906 1905 1904 1903 1902 1901 1900 1999 1998 1997 1996 1995 1994 1993 1992 1991 1990 1989 1988 1987 1986 1985 1984 1983 1982 1981 1980 1979 1978 1977 1976 1975 1974 1973 1972 1971 1970 1969 1968 1967 1966 1965 1964 1963 1962 1961 1960 1959 1958 1957 1956 1955 1954 1953 1952 1951 1950 1949 1948 1947 1946 1945 1944 1943 1942 1941 1940 1939 1938 1937 1936 1935 1934 1933 1932 1931 1930 1929 1928 1927 1926 1925 1924 1923 1922 1921 1920 1919 1918 1917 1916 1915 1914 1913 1912 1911 1910 1909 1908 1907 1906 1905 1904 1903 1902 1901 1900

FIGURE 14

GAGCCGCCGCCGCGCGCGCGCAGCTGCAGCCCCAGGCCGCCACCGTCT
GCGTTGCTGCCCGCCTGGCCAGGCCAAAGGAAGGACAAAGCAGCTGTCAGGGAACCT
CCGCCGGAGTCGAATTACGTGCAGCTGCCGGCAACCACAGGTTCCAAGATGGTTGCGGGG
GCTTCGCGTGTCCAAGAACTGCCTGTGCCCTAACCTGCTTACACCTGGTTAGTCTG
CTGCTAATTGGAATTGCTGCGTGGGCATTGGCTCGGGCTGATTCCAGTCTCCGAGTGGT
CGGCGTGGTCATTGCAGTGGCATCTTCTGTTCTGATTGCTTAGTGGGTCTGATTGGAG
CTGTAACATCATCAGGTGTTGCTATTTTTATATGATTATTCTGTTACTGTATTATT
GTTCAAGTTCTGTATCTGCGCTTGTAGCCCTGAACCAGGAGAACAGGGTCAGCTCT
GGAGGTTGGTTGGAACAATACGGCAAGTGCCTGAAATGACATCCAGAGAAACTAAACTGCT
GTGGGTTCCGAAGTGTAAACCAAATGACACCTGTCTGGCTAGCTGTGTTAAAGTGACCAC
TCGTGCTGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTGAGATTGTTGG
TGGCATTGGCCTGTTCTCAGTTTACAGAGATCCTGGGTGTTGGCTGACCTACAGATA
GGAACCAGAAAGACCCCCCGCGAATCCTAGTGCATTCTTTGATGAGAAAACAAGGAAGAT
TTCCTTCGTATTATGATCTTGTCACTTCTGTAATTTCTGTTAAGCTCCATTGCCAGT
TTAAGGAAGGAAACACTATCTGAAAAGTACCTTATTGATAGTGGAAATTATATTTTACT
CTATGTTCTACATGTTTTCTTCCGTTGCTGAAAATATTGAAACTTGTGGTCTC
TGAAGCTCGTGGCACCTGGAATTACTGTATTGCTGGCCACTGTGGCTT
TCTTAGCATTACCTGCAGAAAAACTTGTATGGTACCACTGTGGTTATATGGTAA
TCTGAACGTACATCTCACTGGTATAATTATGTTAGCAGTGTGCTGTGAGATAGTCC
TGGAAAAAGAGTGGAAATTATTAAATCAGAAAGTATGAGATCCTGTTATGTTAAGGGAAA
TCCAAATTCCAATTGGTCTTTAGGAAAGATTGTTGGTAAAAAGTGTAGTA
AAAAATGATAATTACTGTAGTCTTTATGATTACACCAATGTATTCTAGAAATAGTTAT
GTCTTAGGAAATTGTGGTTAATTGACTTTACAGGTAAGTGCACAGGAGAAGTGGTT
CATGAAATGTTCTAATGTATAATAACATTACCTCAGCCTCCATCAGAACGAGTT
TGAGTAATCAGGAAGTATCTATATGATCTTGATATTGTTATAATAATTGAAAGTCTAA
AAGACTGCATTAAACAAGTTAGTATTAAATGCGTTGGCCCACGTAGCAAAAGATATTG
ATTATCTTAAATTGTTAAATACCGTTTACATGAAATTCTCAGTATTGTAACAGCAACTT
GTCAAAACCTAACGATATTGAATATGATCTCCATAATTGAAATTGAAATCGTATTGTG
GCTCTGTATATTCTGTTAAAAAATTAAAGGACAGAACCTTCTTGTATGCATGTTGA
ATTAAAAGAAAGTAATGGAAG

FIGURE 15

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979
><subunit 1 of 1, 204 aa, 1 stop
><MW: 22147, pI: 8.37, NX(S/T): 3
MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVGVVIAVGIFLFLIALV
GLIGAVKHHQVLLFFYMIILLLVFIVQFSVSCACLALNQEQQGQLLEVGNNTASARNDIQR
NLNCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRFVGGIGLFFSFTEILGVWL
TYRYRNQKDPRANPSAFL
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Signal Peptide:

amino acids 1-34

Transmembrane domains:

amino acids 47-63, 72-95 and 162-182

FIGURE 16

TGATTGGAGCTGTAAAAANTCTTCAGGTGTTGTNATTTTTATATGATTATTCTGTAANT
TGTATTATTGTTCAGTTNTGTATCTTGCCTGTTAGCCNTGAACCAGGAGAACAGG
GTCAGNTNTGGAGGTTGGTGGAAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAAT
NTAAACTGCTGTGGTTCCGAAGTGTAAACCAAATGACACCTGTNTGGCTAGCTGTGTTAA
AAGTGACCACTNGTGCCTGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTGA
GATTGTTGGTGGCATTGGCCTGTTAGTTACAGAGATCCTGGGTGTTGGCTGACC
TACAGATACAGGAACCAG

FIGURE 17

AATCCCAAATTCCCCAATTTTTGGNCTTTAGGGAAAGATGTGTTGTGGTAAAAGTGT
TAGTATAAAAATGATAATTACTTGTAGTCTTTATGATTACACCAATGTATTCTAGAATAG
TTATGTCTTAGGAAATTGTGGTTAATTTGACTTTACAGGTAAGTGCAAAGGAGAAGTG
GTTTCATGAAATGTTCTAATGTATAAACATTACCTTCAGCCTCCCATCAGAATGGAACG
AGTTTGAGTAATCCAGGAAGTATATCTATATGATCTTGATATTGTTTATATAATTGAAG
TCTAAAAGACTGCATTTAAACAAGTTAGTATTAATGCCTGGCCCACGTAGCAAAAGAT
ATTTGATTATCTAAAAATTGTTAAATACCGTTTCATGAAAGTTCTCAGTATTGTAACAGC
AACTTGTCAAACCTAAGCATATTGAATATGATCTCCATAATTTGAAATTGAAATCGTATT
GTGTGGAGGAAATGGCAATCTTATGTGTGCTGAAGGACACAGTAAGAGCACCAAGTTGTGCC
CCACTTGCG

FIGURE 18

ATGATTATTCTGTTACTTGTATTTATTGTTCAGTTTATGGTATCTTGCCTGTTAGCCC
CTGAAACCAGGAGCAACAGGGNNCAGCTTCTGGAGGTTGGCAACAATCACGGCCAAG
TGACTCCGCAAATGACATCCCAGAGAAATCCTAAACTGCTGTGGTTCCGAAGTGTAAACCC
AAATGACACCTGTCTGGCTNGCTGTGTTAAAAGTGACCACTCGTGCTGCCATGTGCTCCAA
TCATAGGAGAATATGC

FIGURE 19

CAGTCACCATGAAGCTGGGCTGTGCCTCATGGCCTGGGCCCTACCTTCCTGGTGTG
CTCTGGGTGGCCCAGATGCTACTGGCTGCCAGTTGAGACGCTGCAGTGTGAGGGACCTGT
CTGCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTGATGCAAGGGAAGCTGGCT
TCCAGGTCAAGGCCTACACTTCACTGAAACCTTCCACCTGATTGTGTCCTATGACTGGCT
ATCCTCCAAGGTCCAGCCAAGCCAGTTGAAGGGGACCTGCTGGTCTGCGCTGCCAGGC
CTGGCAAGACTGCCACTGACTCAGGTGACCTTACCGAGATGGCTCAGCTCTGGTCCCC
CCGGGCCTAACAGGAATTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCACTACCAC
TGCAGTGGCATTTCCAGAGCCCTGGTCTGGATCCCAGAAACAGCATCTGTTGGCTAT
CACAGTCCAAGAACTGTTCCAGCGCAATTCTCAGAGCTGTACCCCTCAGCTGAACCCCAAG
CAGGAAGCCCCATGACCCCTGAGTTGTCAAGACAAAGTTGCCCTGCAGAGGTCA
CTCCTCTCTCCTTCTACAAGGATGGAAGGATAGTCAAAGCAGGGGCTCTCCTCAGAATT
CCAGATCCCCACAGCTCAGAAGATCACTCCGGGTCAACTGGTGTGAGGCAGCCACTGAGG
ACAACCAAGTTGGAAACAGAGCCCCCAGCTAGAGATCAGAGTCAGGGTCTCCAGCTCT
GCTGCACCTCCCACATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGA
GGAGGCCCTGGCCTCGCCTCGCCGCCAACCCATCTCTGAGGATCCAGGCTTTCTT
CTCCTCTGGGATGCCAGATCCTCATCTGTATCACCAGATGGCCTTCTCAAACACATG
CAGGATGTGAGAGTCCTCGGTACCTGCTCATGGAGTTGAGGAATTATCTGGCCACCA
GAAGCCTGGGACCACAAAGGCTACTGCTGAATAGAAGTAAACAGTT
CATCCATGATCTCACTTAACACACATG
TAACCACCCAAATAATCTGATTCTTATTTCTCTCCTGTCCTGCACATATGCATAAGTA
CTTTTACAAGTTGTCCTCAGTGTGTTGTTAGAATAATGTAGTTAGGTGAGTGTAA
ATAAAATTT
ATATAAAAGTGAGAATTAGAGTTAGCTATAATTGTGTATTCTCTCTTAACACACAGAATT
TGCTGTCTAGATCAGGAATTCTATCTGTATATCGACCAGAATGTTGTGATTAAAGAGAA
CTAATGGAAGTGGATTGAATAACAGCAGTCTCAACTGGGGCAATT
TTGGGCAATGTTGGAGACATTGTCATTATACTTGGGGTGGGATGGTGGGATGT
GTGTCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCCTAAACATCCTATAATGCACAG
GGCAGTACCCACACGAAAATAATCTGGCCAAAATGTCAGTTGACTGAGTTGAGAAA
CCCCAGCCTAATGAAACCCCTAGGTGTTGGCTCTGGAATGGACTTGTCCCTCTAATT
TATCTCTTCCAGCCTCATTCACTATTCTACTGACATACCAGTCTTAGCTGGTGTATG
GTCTGTTCTTAGTTGTTAGCTAAAGCCATTATGTTGAAATCCTAATCCCC
AAGGTGATGGCATTAAAGAAGTGGCCTTGGGAAGTGATTAGATCAGGAGTGCAGAGCCCTC
ATGATTAGGATTAGTGCCTTATTAAAAAGGCCAGAGAGCTA
ACTCACCCTCACC
ATGAGGACGTGGCAAGAAGATGACATGTATGAGAACCAAAAAACAGCTGTCGCCAAACACCG
ACTCTGTCGTTGCCTTGATCTGAACCTCCAGCCTCCAGAACTATGAGAA
ATAAAATTCTGG
TTGTTGTAGCCTAA

FIGURE 20

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594
><subunit 1 of 1, 359 aa, 1 stop
><MW: 38899, pI: 5.21, NX(S/T): 0
MKLGCVLMAWALYLSLGVLWVAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQV
KAYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRCQAWQDWPLTQVTFYRDGSALGPPGP
NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGS
PMTLSCQTKLPLRSAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHGSYWCEAATEDNQ
VWKQSPQLEIRVQGASSSAAPPTLNPAQKSAAPGTAPEEAPGPLPPPPTPSSEDPGFSSPL
GMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE
```

Signal sequence:

amino acids 1-17

Leucine zipper pattern sequence:

amino acids 12-33

Protein kinase C phosphorylation site:

amino acids 353-355

FIGURE 21

CCCACGCGTCCGCCACGCGTCCGCCACGGGTCCGCCACGCGTCCGGCCACCAGAAGTT
TGAGCCTTTGGTAGCAGGAGGCTGGAAGAAAGGACAGAAAGTAGCTCTGGCTGTG**AT**GGGG
ATCTTACTGGGCTGCTACTCCTGGGCACCTAACAGTGGACACTTATGGCGTCCCACCT
GGAAGTGCCAGAGAGTGTAAACAGGACCTTGGAAAGGGATGTGAATCTCCCTGCACCTATG
ACCCCTGCAAGGCTACACCCAAGTCTTGGTGAAGTGGCTGGTACAACGTGGCTCAGACCC
GTCACCATCTTCTACGTGACTCTCTGGAGACCATATCCAGCAGGCAAAGTACCAAGGGCG
CCTGCATGTGAGCCACAAGGTTCCAGGAGATGTATCCCTCCAATTGAGCACCCCTGGAGATGG
ATGACCGGAGCCACTACACGTGTGAAGTCACCTGGCAGACTCCTGATGGCAACCAAGTCGTG
AGAGATAAGATTACTGAGCTCGTGTCCAGAAACTCTCTGTCTCCAGCCCACAGTGACAAC
TGGCAGGGTTATGGCTCACGGTCCCCAGGGAAATGAGGATTAGCCTCAATGCCAGGCTC
GGGGTTCTCCTCCCACAGTTATTTGGTATAAGCAACAGACTAATAACCAGGAACCCATC
AAAGTAGCAACCTTAAGTACCTTACTCTCAAGCCTGCGGTGATAGCCACTCAGGCTCCTA
TTTCTGCACTGCCAAGGGCCAGGTTGGCTTGAGCAGCACAGCAGCATTGTGAAGTTGTGG
TCAAAGACTCCTCAAAGCTACTCAAGACCAAGACTGAGGCACCTACAACCATGACATACCC
TTGAAAGCAACATCTACAGTGAAGCAGTCCTGGACTGGACACTGACATGGATGGCTACCT
TGGAGAGACCAGTGCTGGGCCAGGAAAGAGCCTGCGTGTCTTGCATCATCCTCATCATCT
CCTTGTGCTGTATGGGTTTACCATGGCTATATCATGCTCTGCGGAAGACATCCCAA
CAAGAGCATGTCTACGAAGCAGCCAGG**TA**AGAAAGTCTCCTCTCCATTGGACCCGT
CCCTGCCCTCAATTGGTACTGGCAGGAAATGTGGAGGAAGGGGGGTGTGGCACAGACCC
AATCCTAAGGCCGGAGGCCTTCAGGGTCAGGACATAGCTGCCCTCCCTCTCAGGCACCTT
CTGAGGTTGTTGGCCCTCTGAACACAAAGGATAATTAGATCCATCTGCCCTCTGCTTCC
AGAATCCCTGGGTAGGATCCTGATAATTAAATTGGCAAGAATTGAGGCAGAAGGGTGGGA
AACCAGGACACAGCCCCAAGTCCCTCTTATGGGGGTGGCTTGGCCATAGGGCACA
TGCCAGAGAGGCCAACGACTCTGGAGAAACCATGAGGGTGGCATCTCGCAAGTGGCTGCT
CCAGTGATGAGCCAACCTCCCAGAATCTGGCAACAACACTCTGATGAGCCCTGCATAGGA
CAGGAGTACAGATCATGCCAGATCAATGGCAACTACGCCGCTGGACACAGTTCC
TCTGGATTATGAGTTCTGGCCACTGAGGGCAAAGTGTCTGTTAAAATGCCCTTAGGC
CAGGATCTGCTGACATAATTGCCCTAGTCAGTCCTGCCCTCTGCATGGCCTCTCCCTGCT
ACCTCTCTCCTGGATAGCCAAAGTGTCCGCTACCAACACTGGAGCCGCTGGAGTCAC
GGCTTGCCCTGGAATTGCCAGATGCATCTCAAGTAAGCCAGCTGCTGGATTGGCTCTGG
GCCCTCTAGTATCTGCCGGGGCTTCTGGTACTCCTCTAAATACCAAGAGGGAAAGATG
CCCATAGCACTAGGACTTGGTCATCATGCCCTACAGACACTATTCAACTTGGCATCTGCCA
CCAGAAGACCCGAGGGAGGCTCAGCTGCCAGCTCAGAGGACCAAGCTATATCCAGGATCAT
TTCTCTTCTTCAGGGCCAGACAGCTTTAATTGAAATTGTTATTCACAGGCCAGGGTTCA
GTTCTGCTCCTCCACTATAAGTCTAATGTTCTGACTCTCCTGGTGTCAATAAATATCTA
ATCATAACAGC

FIGURE 22

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45416
><subunit 1 of 1, 321 aa, 1 stop
><MW: 35544, pI: 8.51, NX(S/T): 0
MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCPTYDPLQGYTQVLVKWLVQRGS
DPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQ
VVRDKITELRVQKLSVSKPTVTTGSGYGFVHQGMRISLQCQARGSPPISYIWYKQQTNNQE
PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKEAPTTMT
YPLKATSTVKQSWDWTTDMGYLGETSAGPGKSLPVFAIILIISLCCMVVFTMAYIMLCRKT
SQQEHVYEAAR
```

Signal Sequence:

amino acids 1-19

Glycosaminoglycan attachment site:

amino acids 149-152

Transmembrane domain:

amino acids 282-300

FIGURE 23

CGGCCGGGAGCCCATCTGCCCGAGGGCACGGGGCGCGGGCGCTCCGCCGGCACAT
GGCTGCAGCCACCTCGCGCGACCCCGAGGCAGCCGCAGCTCGCCCGAGGTCCCGTCGGA
GGCAGCCGGCGCCCGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCTCCGGGATC
GGGATGTCCCTCCTCCTCTCTCTTGCTAGTTCTACTATGTTGAACTTGGGACTCA
CACTGAGATCAAGAGAGTGGCAGAGGAAAGGTCACTTGCCCTGCCACCATCAACTGGGC
TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACAAAAA
GTGGTGATCACTTACTCCAGTCGTATGTCTACAATAACTGACTGAGGAACAGAACAGGGCG
AGTGGCCTTGTCTCCAATTTCCTGGCAGGAGATGCCTCTGCAGATTGAACCTCTGAAGC
CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTAGGGCGCTACGTGTGGAGGCCAT
GTCATCTTAAAGTCTTAGTGAGACCATCCAAGCCAAGTGTGAGTTGGAAGGAGAGCTGAC
AGAAGGAAGTGAACCTGACTTGAGTCAGTGTGAGTCATCCTCTGGCACAGAGCCATTGTGATT
ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGTGAACGTCTGCCTCCAAATCTAGGATT
GACTACAACCACCCCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCTACTCTGGACTGTA
CCAGTGCACAGCAGGCAACGAAGCTGGAAAGGAAGCTGTGAGTCAGTAACGTACAGT
ATGTACAAAGCATCGGCATGGTGTGGCAGGAGCAGTGCAGGACATAGTGGCTGGAGCCCTGCTG
ATTTCTCTGGTGTGGCTTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA
GAGACCTAATGAAATTGAGAAGATGCTGAAGCTCCAAAGCCGCTTGTGAAACCCAGCT
CCTCTCCTCAGGCTCTCGGAGCTCACGCTCTGGTCTTCCACTCGCTCCACAGCAAAT
AGTGCCTCACGAGCCAGCGGACACTGTCAACTGACGAGCACCCAGCCAGGGCTGGCAC
CCAGGCATACAGCCTAGTGGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATG
CTAATCTGACCAAAGCAGAACACACCCAGCATGATCCCCAGCCAGAGCAGGCCTCCAA
ACGGTCTGAATTACAATGGACTTGACTCCCACGCTTCTAGGAGTCAGGGCTTGGACTC
TTCTCGTCATTGGAGCTCAAGTCACCAGGCACACAACCAGATGAGGAGGTCTAAGTAGCA
GTGAGCATTGCAAGGAACAGATTAGATGAGCATTTCTTACAAATACCAAACAGCAA
AGGATGTAAGCTGATTCATCTGAAAAAGGCATCTTATTGTGCTTAGACCAGAGTAAGGG
AAAGCAGGAGTCCAAATCTATTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGAAAGGTG
AGGTGAATATACCTAAACTTTAATGTGGATATTGTATCAGTGTCTTGATTACAATT
TTCAAGAGGAATGGATGCTTTGTAATTCTATGCATTCTGCAAACATTATTGGATT
ATTAGTTATTCAAGACAGTCAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC
TGAGCTAACCACTCTAACAAACTCCAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC
TTCAAGGTTGGATATTAAATTCAAGGGAGGTGAAATAGTGGAGATGGAGA
AGAGTGAATGAGTTCTCCACTCTATAACTATCTCACTATTGTATTGAGCCAAAATAAC
TATGAAAGGAGACAAAATTGTGACAAAGGATTGTGAAGAGCTTCCATCTCATGTT
ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTCCCTCAAAT
CAGATGCCTCTAAGGACTTCTGCTAGATATTCTGGAAGGAGAAAATACAACATGTCATT
TATCAACGTCTTAGAAAGAATTCTCTAGAGAAAAGGGATCTAGGAATGCTGAAAGATTA
CCCAACATACCATTATAGTCTCTTCTGAGAAAATGTGAAACCCAGAAATTGCAAGACTGG
GTGGACTAGAAAGGGAGATTAGATCAGTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA
TGGTGCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGGTGCAAGTGCAGGCCAGATTATGCC
ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

FIGURE 24

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41281, pI: 8.33, NX(S/T): 3
MSLLLLLLVSYYVGTGLTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPCKELEGELTEGSDLTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMYSGLYQCTAGNEAGKESCVVVRTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKEYEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRGSSSTRSTANS
ASRSQRTLSTDAAAPQPGLATQAYSLVGPEVRGSEPKVHHANLTKAETTPSMIPSQSRAFQTV
```

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

FIGURE 25

GTCGTTCTTGTCTCTCGCGCCAGTCCTCCCTGGTCTCCTCAGCCGCTGCGAGGAGAGCACCCGGA
GACGCGGGCTGCACTCGCGGGCTTCCTCCCCGCTGGCGGCTCGCCGCTGGCAGGTGCTGAGCAGCCCTAG
AGCCTCCCTGCGCCCTCCCTCTGCCCGGCCAGCAGTCACATGGGGTGTGGAGGTAGATGGGCTCCG
GCCCGGGAGGCGCGGTGGA TGCGCGCTGGCAGAAGCAGCCGATTCCAGTGCCTCGCCGCGCCCCGGCG
CCCCCTGCGAGTCCCCGGTCAGCCATGGGGACCTCTCGAGCAGCAGCACGCCCTGCCCTCTGCAGCCGCATC
GCCCGCCGAGCCACAGCACCGATGATCGGGCTCCCTCTCTGCTGGATTCTTAGCACCACAGCTCAG
CCAGAACAGAACAGGCTCGAATCTCATTGGCACATACGCCATGTTGACCGTGCACCAGGTGCTAACCTGT
GACAAGTGTCCAGCAGGAACCTATGTCTGAGCATTGTACCAACACAAGCCTGCGCTGAGCAGTTGCCCT
GTGGGGACCTTACCAAGGCATGAGAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCATGCCAATG
ATTGAGAAATTACCTTGTGCTGCTTGAUTGACCGAGAATGCACGTGCCACCTGGCATGTTCCAGTCTAACGCT
ACCTGTGCCCTACGGTGTGCTGTGGTTGGGTGTGCGGAAGAAAGGGACAGAGACTGAGGATGTGCGG
TGTAAGCAGTGTGCTGGGTACCTTCAGATGTGCTTAGTGTGATGAAATGCAAAGCATACACAGACTGT
CTGAGTCAGAACCTGGTGGTATCAAGCCGGGACCAAGGAGACAGACAACGTCTGTGGCACACTCCGTCCTTC
TCCAGCTCCACCTCACCTCCCTGGCACAGCCATCTTCCACGCCCTGAGCACATGAAACCCATGAAGTCCCT
TCCTCCACTTATGTTCCAAAGGCATGAACTCAACAGAACATCCAACCTCTGCCCTGTTAGACCAAAAGGTACTG
AGTAGCATCCAGGAAGGGACAGTCCCTGACAACACAAGCTCAGCAAGGGGAGGAAGACGTGAACAAAGACCC
CCAAACCTTCAGGTAGTCACACCAGCAAGGCCACACAGAACATCCTGAAGCTGCTCCGTCCATGGAG
GCCACTGGGGCGAGAACGTCCAGCACGCCCATCAAGGCCACAGAGGGGACATCCTAGACAGAACCTACACAAG
CATTGTGACATCAATGAGCATTGCCCTGGATGATTGTGCTTTCTGCTGCTGGTCTGTGGTGAATTGGTGG
TGCAGTATCCGAAAAGCTCGAGGACTCTGAAAAAGGGGCCGGCAGGATCCAGTGCCTTGTGGAAAAGGCA
GGGCTGAAGAAATCCATGACTCCAACCCAGAACCGGGAGAAATGGATCTACTACTGCAATGCCATGGTATCGAT
ATCCTGAAGCTTGTAGCAGCCAAGTGGGAAGCCAGTGGAAAGATATCTATCAGTTCTTGAATGCACTGAG
AGGGAGGTTGCTGCTTCTCAATGGGTACACAGCCGACCACGAGCGGCCCTACCCAGCTCTGCAGCACTGGACC
ATCCGGGCCCGAGGCCAGCCTGCCAGCTAAATTAGGCCCTGCCAGCACCGGAGAACAGATGTGTGGAG
AAGATTGTTGGCTGATGGAAGACACCACCCAGCTGAAACTGACAAACTAGCTCTCCGATGAGCCCCAGCCCG
CTTAGCCGAGCCCCATCCCCAGCCCCACGCAGAACACTTGAGAATTCCGCTCTCTGACGGTGGAGCCTCCCCA
CAGGACAAGAACAGGGCTTCTCGTGGATGAGTCGGAGGCCCTCTCGCTGTACTCTACATCCAGGGCTCC
TCCGCGCTGAGCAGGAACGGTCTTTATTACAAAGAAAGAACAGTGTGCGGCAGGTACGCCCTGGAC
CCCTGACTTGCAGCCTATTTGATGACATGCTCCACTTCTAAATCTGAGGAGCTGCCGTGATTGAAGAG
ATTCCCCAGGCTGAGGACAAACTAGACCGCTATTGAAATTATTGGAGTCAGAGGCCAGGAAGCCAGCAGACC
CTCTGGACTCTGTTATAGCCATCTTCTGACCTGCTGTAAGACATAGGGATACTGCAATTCTGAAATTACTCA
ATTAGTGGCAGGGTGGTTTTAATTCTCTGTTCTGATTTTGTGTTGGGTGTGTGTGTTGT
GT
TCTCTCTCTTTTTAAATAACTCTCTGGGAAGTGGTTATAAGCCTTGGCCAGGTGTAACTGTTCTCTCTCTC
ATACCCACCAACTAAAGTTTAAAGTCCATATTCTCCATTGCTTCTGTTATGTTCAAGATTACTG
TGCACCTAAATTACTAACATACCAAAATGCACTGTAACCTTCCCACACACTGGATTGTGAGGCTTAAAC
TTCTAAAGTATAATGCCATCTGTGAATCCTATAAGCAGTCTTATGTCCTAACATTACACACTTCTT
AAAAACAAATATTACTATTATTGTTGTCTTTATAAATTCTTAAAGATTAAGAAAATTAAAGA
CCCCATTGAGTTACTGAAATGCAATTCAACTTGTAGTTATCTTTAAATATGTCCTGTATAGTCATATTG
CTGAAACTGACCACACTATTGCTGATGTTATGTTTCACTGGACACCGTGTAGAATGCTGATTACTGTAC
TCTTCTTATGCTAATATGCTGGCTGGAGAAATGAAATCCTCAAGCCATCAGGATTGCTATTAAAGTGGCTT
GACAACGGGCCACCAAAGAACCTGAACTTCACCTTTAGGATTGAGCTGTTCTGGAACACATTGCTGCACTT
GGAAAGTCAAATCAAGTGCAGTGGGCCCTTCCATAGAGAATTGCCCAGCTTGTCTTAAAGATGTCTG
TTTTTATATACACATAATCAATAGGTTCAATCTGCTCTCAAGGCCCTGGTCTGGTGGGATTCTTCAACCAATT
ACTTTAATTAAAAATGGCTGCAACTGTAAGAACCTTGTCTGATATATTGCAACTATGCTCCATTACAAATG
TACCTTCTAATGCTCAGTTGCCAGGTTCAATGCAAAGGTGGCGTGGACTCCCTTGTGTGGTGGGTTGTGG
GTAGTGGTGAAGGACCGATATCAGAAAATGCCCTCAAGTGTACTAATTATTAATAACATTAGGTGTTGTTA
AAAAAA

FIGURE 26

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594
><subunit 1 of 1, 655 aa, 1 stop
><MW: 71845, pI: 8.22, NX(S/T): 8
MGTSPSSSTALASCRIARRATATMIAGSLLLLGFLSTTTAQPEQKASNLIGTYRHVDRATG
QVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFRHENGIEKCHDCSQPCPWPMLIEKLPKA
ALTDRECTCPPGMFQSNTCAPHTVCAPVGWGVKKGTETEDVRCKQCARGTFSDVPSSVMKC
KAYTDCLSQNLVVIKPGTKETDNVCGTLPSFSSSTSPSPGTIAIFPRPEHMETHEVPSSTYVP
KGMNSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVNVHQQGPHHRHIL
KLLPSMEATGGEKSSTPIKGPKRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVVIIVVCSIRK
SSRTLKKGPRQDPSAIVEKAGLKKSMTPTQNREKWIYYCNGHGIDILKLVAAQVGSQWKDIY
QFLCNASEREVAAFSNGYTADHERAYAALQHWTIRGPEASLAQLISALRQHRRNDVVEKIRG
LMEDTTQLETDKLALPMSPSPLSPSPPIPSNAKLENSALLTVEPSPQDKNKGFFVDESEPLL
RCDSTSSGSSALSRNGSFITKEKKDTVLRQVRLDPQLQPIFDDMLHFLNPEELRVIEEIPQ
AEDKLDRRLFEIIGVKSQEASQTL LDSVYSHLPDLL
```

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 350-370

FIGURE 27

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCCGTGGTGCATCTACATTGGGA
CTCGGGATTATGAGGTAGAGGTGGAGGCCGGATGTCAGAGGTCTGAAATAGTCAC
CATGGGGAAAATGATCCGCCTGCTGTTGAAGCCCCCTCTCATTCCGATCGCTTTGGCC
TTGATGATTGAAAATAAGTCCTGTTGACCAAGATGCAAGATGCTGTTGCTGCACAGATCCTG
TCACTGCTGCCATTGAAGTTTTCCAATCATCGTCATTGGATCATTGCATTGATATTAGC
ACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGAAGTACAGATGTCGCTCATCCT
TTAAGTGTATCGAGCTGATAGCTGATGTGACGGAGTCTGGATTGCAAAGACGGGGAGGAC
GAGTACCGCTGTCGGGTGGGTGGTCAGAATGCCGTGCTCCAGGTGTTACAGCTGCTTC
GTGGAAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAATGTTGCCTGTGCCAAC
TGGTTTCCAAGCTATGTGAGTTCAGATAACCTCAGAGTGAGCTCGCTGGAGGGCAGTTC
CGGGAGGAGTTGTGTCATCGATCACCTCTGCCAGATGACAAGGTGACTGCATTACACCA
CTCAGTATATGTGAGGGAGGGATGTGCTCTGCCACGTGGTTACCTGCAGTGCACAGCCT
GTGGTCATAGAAGGGGCTACAGCTCACGCATCGTGGTGGAAACATGTCCTGCTCGCAG
TGGCCCTGGCAGGCCAGCCTCAGTTCCAGGGCTACCACTGTGCCGGGCTCTGTCATCAC
GCCCTGTGGATCATCACTGCTGCACACTGTGTTATGACTTGTACCTCCCAAGTCATGGA
CCATCCAGGTGGTCTAGTTCCCTGTTGGACAATCCAGCCCCATCCCACTGGTGGAGAAG
ATTGTCTACCACAGCAAGTACAAGCCAAAGAGGCTGGCAATGACATGCCCTATGAAGCT
GCCGGGCCACTCACGTTCAATGAAATGATCCAGCCTGTGCTGCCAACTCTGAAGAGA
ACTTCCCCGATGGAAAAGTGTGCTGGACGTCAAGGATGGGGGCCACAGAGGATGGAGGTGAC
GCCTCCCTGTCTGAACCACGCCGTCCTTGATTCCAACAAGATGCAACCACAG
GGACGTGTACGGTGGCATCATCTCCCCCTCATGCTCTGCCGGCTACCTGACGGTGGCG
TGGACAGCTGCCAGGGGACAGCGGGGCCCTGGTGTGTCAGAGAGGAGGTGTTGGAAG
TTAGTGGAGCGACCAGCTTGGCATCGCTGCGCAGAGGTGAACAAGCCTGGGTGTACAC
CCGTGTACCTCCTGGACTGGATCCAGCAGCAGATGGAGAGAGACCTAAAAACTGAA
GAGGAAGGGACAAGTAGCCACCTGAGTCCTGAGGTGATGAAAGACAGCCGATCCTCCCT
GGACTCCCGTAGGAAACCTGCACACGAGCAGACACCCTGGAGCTGAGTTCCGGCACCA
GTAGCAGGCCGAAAGAGGCACCCCTCATCTGATTCCAGCACAAACCTCAAGCTGCTTTT
GTTTTTGTGTTGGAGGTGGAGTCTCGCTCTGTTGCCAGGCTGGAGTGCAGTGGCGAAA
TCCCTGCTCACTGCAGCCTCCGCTTCCCTGGTTCAAGCGATTCTGCCTCAGCTCCCA
GTAGCTGGACACAGGTGCCGCCACACACCCAACTAATTTGTATTTAGTAGAGAC
AGGGTTCACCATGTTGCCAGGCTGCTCAAACCCCTGACCTCAAATGATGTGCCTGCTT
CAGCCTCCCACAGTGTGGATTACAGGCATGGGCCACCGCCTAGCCTACGCTCCTTTC
TGATCTCACTAAGAACAAAAGAAGCAGCAACTTGCAAGGGCGGCTTCCACTGGTCCAT
CTGGTTTCTCCAGGGTCTGCAAATTCTGACGAGATAAGCAGTTATGTGACCTCAG
TGCAAAGCCACCAACAGCCACTCAGAAAAGACGCACCAGCCAGAAGTGCAGAACTGCAGTC
ACTGCACGTTTCATCTCTAGGGACCAACCAACCCACCCCTTCTACTTCCAAGACTTAT
TTTCACATGTGGGAGGTTAATCTAGGAATGACTCGTTAAGGCCTATTTCATGATTCTT
TGTAGCATTGGTGTGACGTATTATTGTCCTTGATTCCAAATAATATGTTCCCTCCCT
CATTGTCTGGCGTGTGCGTGGACTGGTGACGTGAATCAAATCATCCACTGAAA

FIGURE 28

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234
><subunit 1 of 1, 453 aa, 1 stop
><MW: 49334, pI: 6.32, NX(S/T): 1
MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALILA
LAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVFTAAS
WKTMCSDDWKGHYANVACAQLGFPSSYVSSDNLRVSSLEQFREFVSIDHLLPDDKVTALHH
SVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVIT
PLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKL
AGPLTFNEMIQPVCLPNEENFPDGKVCWTSGWGATEDGGDASPVLNHAAPLISNKICNHR
DVYGGIISPSMLCAGYLTDGGVDSCQGDGGPLVCQERRLWKLVGATSGIGCAEVNKPGVYT
RVTSFLDWIHEQMERDLKT
```

Signal Peptide:

amino acids 1-20

Transmembrane domain:

amino acids 240-284

FIGURE 29

CCACCGCGTCCGTCTAGTCCCCGGCCAACCGAACAGTTGCTCATTATTGCAACGGTCAAGGCTGGCTTGT
GCCAGAACGGCGCGCGCGCGCACGCACGCACACACACGGGGGGAAACTTTTAAAAATGAAAGGCTAGAAGA
GCTCAGCGGGCGCGCGGGCGCTCGCGAGGGCTCCGGAGCTGACTCGCCGAGGCAGGAAATCCCTCCGGTCGCGA
CGCCCGGCCCCGGCTCGCGCCCCCGTGGGATGGTGAGCGCTCGCCGCCGGCCCGAGAGCTGCTGCACTGAAG
GCCGGCGACGATGGCAGCGCGCCCGCTGCCGTGCCCCGCCGCCCTCCTGCTGCCCTGGCCGGTGTCT
GCTCGGCCCTCGAGGGCCGAGGGGTGAGCTTATGAAACCAAGGAAGAGCTGATGAAGTTGTCAGTGCCTCTGT
TCGGAGTGGGACCTCTGGATCCCAGTGAAGAGCTCGACTCCAAGAATCATCCAGAAGTGTGAATATCGACT
ACAACGGGAAAGCAAAGAACTGATCATAAATCTGAAAGAAATGAAGGTCTATTGCCAGCAGTTCACGAAAC
CCACTATCTGCAAGACGGTACTGATGTCTCCCTCGCTCGAAATTACACGGGTCACTGTTACTACCATGGACATGT
ACGGGGATATTCTGATTCAAGCAGTCAGTCTCAGCACGTGTTCTGGTCTCAGGGACTTATTGTGTTGAAATGA
AAGCTATGCTTCTAGAACCAATGAAAGTGAACCAACAGATAACAAACTCTCCAGCGAAGAAGCTGAAAGCGT
CCGGGATCATGTGGATCACATCAACACACCAAAACCTCGCTGCAAAGAATGTGTTCCACCACCCCTCTCAGAC
ATGGGCAAGAAGGCATAAAAGAGAGACCCCTCAAGGCAACTAAGTATGTGGAGCTGGTATCGTGGCAGACAACCG
AGAGTTTCAGAGGCAAGGAAAAGATCTGGAAAAAGTTAAGCAGCGATTAAAGAGATGCTAATCACGTTGACAA
GTTTACAGACCACTGAACATTGGATCGTGTGGTAGGGCTGGAAGTGTGGAATGACATGGACAAATGCTCTGT
AACTCAGGACCCATTCAACCACCTCCATGAAATTCTGGACTGGAGGAAGATGAAGCTCTACCTCGCAAATCCCA
TGACAATGCGCAGCTGTGAGTGGGTTTATTCCAAGGGACCCATCGGATGGCCCAAATCATGAGCATGTG
CACGGCAGACCGACTCTGGGGAAATTGTGATGGACCATTCAGACAATCCCTGGTGCAGCGTGACCCCTGGCACA
TGAGCTGGGCCACAATTCTGGGATGAATCATGACACACTGGACAGGGCTGTAGCTGCTCAAATGGCGTTGAGAA
AGGAGGCTGCATCATGAAACGCTTCCACGGGTACCCATTCCATGGTGTGAGCAGTTGCAAGCAGGAAGGACTT
GGAGACCAGCCTGGAGAAAGGAATGGGGTGTGCGCTTTAACCTGCCGAACTCAGGGAGTCTTCGGGGGCCA
GAAGTGTGGAACAGATTGTGAGAAGAGGAGGGAGTGTGACTGTGGGAGGCCAGAGGAATGTATGAATCGTGT
CTGCAATGCCACCACCTGTACCCCTGAAGCCGGACGCTGTGCGCACATGGCTGTGCTGAAAGACTGCCAGCT
GAAGCCTGCAGGAACACCGTGCAAGGACTCCAGCAACTCCTGTGACCTCCAGTCTGCACAGGGCCAGCCC
TCACTGCCAGCCAATGTGTACCTGCACGATGGCACTCATGTCAGGATGTGGACGGCTACTGCTACAATGGCAT
CTGCCAGACTCACGAGCAGCAGTGTGTCACGCTCTGGGGACAGGTGCTAACCTGCCCTGGATCTGCTTGA
GAGAGTCATTCTGAGGTATGCCACTGTGCAAAGTCTGCAAGAGTTCTTGCCAAATGCCAGAT
GAGAGATGCTAAATGTGGAAAATCCAGTGTCAAGGAGGTGCCAGCCGGCAGTCATTGGTACCAATGCCTTTC
CATAGAAACAAACATCCCTCTGAGCAAGGAGGCCGATTCTGTGCCGGGGACCCACGTGTACTTGGCGATGA
CATGCCGGACCCAGGGCTTGTGCTGAGGCACAAAGTGTGCAAGATGGAAAATCTGCCCTGAATCGTCAATGTCA
AAATATTAGTGTCTTGGGTTACGAGTGTGCAATGCACTGTCACGGCAGAGGGGTGTGCAACAAACAGGAAGAA
CTGCCACTCGAGGCCACTGGCACCTCCCTCTGTGACAAGTTGGCTTGGAGGAAGCAGACAGCAGGGCCC
CATCCGGCAAGCAGAACAGGAGGAGTCAGGCAACAGGGCCGAGGGAGGCCAGGGAGGCCAGGGAGCCCTGGG
ATCGCAGGAGGATGCGTCACTGCCACTGACACTCATCTGAGCCTCCCATGACATGGAGACCGTGACAGTG
CTGCTGAGAGGAGGTACCGTCCCCAAGGCCCTCTGTGACTGGCAGCATTGACTCTGTGGCTTGGCATCGTT
TCCATGACAACAGACACACACAGTTCTGGGCTCAGGAGGGAAAGTCCAGCCTACAGGACAGTCTGCAGAAA
CAGTGCAGGAAGGGCAGCAGTCTGGTTGAGCTCTGCTAAACATGGACATGCTCAGTGTCTGCTCTGAG
AGAGTAGCAGGTTACCACTCTGGCAGGCCAGGCCCTGAGCAAGGAGGAAGGACTCAAAAGTCTGCCCTTC
ACTGAGCCTCCACAGCACTGGGAGAAGCAAGGGTTGGGCCAGTGTCCCTTCCCAGTGCACACCTCAGCCT
TGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTGTGATATGGCTTTAGCATTTATTATGAAAAT
AGCAGGGTTTAGTTTAATTATCAGAGACCCCTGCCACCCATTCCATCTCCATCCAAGCAAACGCTAATGGCAA
TGAAACAAACTGGAGAAGAAGGAGGAGAAGGGCGGTGAACCTGGCTTTGCTGTGGACATGCGTGACCAGC
AGTACTCAGGTTGAGGGTTGAGAAAGCCAGGGACCCACAGAGTCACCAACCTCATTAAACAAGTAAGAA
TGTAAAAAGTGAACAAATGTAAGAGCCTAATCCATCCCCGTGGCCATTACTGCATAAAATAGAGTGCATTT
GAAAT

FIGURE 30

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624
><subunit 1 of 1, 735 aa, 1 stop
><MW: 80177, pI: 7.08, NX(S/T): 5
MAARPLPVSPARALLLAGALLAPCEARGVSLWNQGRADEVVSASVRSGDLWIPVKSFDISK
NHPEVLNIRLQRESKELIINLERNEGLIASSFTETHYLQDGTDVSLARNYTGHCYYGHVRG
YSDSAVSLSTCGLRGLIVFENESYVLEPMKSATNRYKLFPAKKLKSVRGSCGSHNTPNLA
AKNVFPPPSQTWARRHKRETLKATKYVELVIVADNREFQRQGKMLEVKQRLIEIANHVDKF
YRPLNIRIVLVGVEWNDMDKCSVQDPFTSLHEFLDWRKMKLLPRKSHDNAQLVSGVYFQG
TTIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNFGMNHDTLDRGCSCQMAVEK
GGCIMNASTGYPFPMPVFSSCSRKDLETSLEKGMGVCLFNLPEVRESFGGQKCGNRFVEEGEE
CDCGEPEECMNRCNATTCTLKPDAVCAHGLCCEDCQLKPAGTACRDSSNSCDLPEFCTGAS
PHCPANVYLHDGHSCQDVGYCYNGICQTHEQQCVTLWPGPAKAPGICFERVNSAGDPYGN
CGKVKSSFAKCEMRDAKCGKIQCQGGASRPVIGTNAVSIEETNIPLQQGGRILCRGTHVYLG
DDMPDPGLVLAGTKCADGKICLNRQCQNISVFGVHECAMQCHGRGVNNRKNCHCEAHWAPP
FCDKFGFGGGSTDGPIRQAEARQEEAESNRERGQGQEPVGSQEHASTASLTLI
```

Signal peptide:

amino acids 1-28

FIGURE 31

TCCCAAGGCTTCTGGATGGCAGATGATTNTGGGTTTGCATTGTTCCCTGACAACGAAA
ACAAAACAGTTGGGGTTCAAGGAGGGAAANTCCAGCCTACCCAGGAAGTTGCAGAAACAA
GTGCAAGGAAGGGCAGGANTCCTGGTTGAGNTTTGNTAAAACATGGACATGNTTCAGTG
CTGCTCNTGAGAGAGTAGCAGGTTACCACTTTGGCAGGCCAGGCCCTGCAGCAAGGAGGA
AGAGGAAGTCAAAAGTTGGCCTTCACTGAGCCTCACAGCAGTGGGGAGAAGCAAGGGTT
GGGCCAGTGTCCCCTTCCCCAGTGACACCTCAGCCTGGCAGCCCTGATAACTGGTNTNT
GGCTGCAANTTAATGCTNTGATATGGCTTTAGCATTATTATGAAAATAGCAGGGTTT
AGTTTTAATTATCAGAGACCTGCCACCCATTCCATNTCCATCCAAG

ପାତା ୧୦୦

FIGURE 32

CATCCTGCAACATGGTAAACCACGCCTGGCTAATTTGTTGTTAGAGATGGGA
TTTCACCGTGTAGCCAGGATTGCTCAATCTGACCTCATGATCTGCCCGCTCGGCCTCCC
AAAGTGCCTGGATTACAGCGAGTGCAACCACACCCGGCCACAAACTTTAAGAAGTTAAT
GAAACCATACTTTACATTTAATGACAGGAAAATGCTCACAATAATTGTTAACCCAAA
TTCTGGATACAAAAGTACAATCTTACTGTGTAATACATGTATATGTTACTATGAAAATA
TACCAAATATCAATAACTTATCTGGTAAAAACCTCTCATACCCTGTGCTAACAA
CTTTAACAAAAAATTGCATCACTTTAAGAATCAAGAAAAATTCTGAAGGTATATGGG
ACAGAAAAAAACCAAGGGAAAATCACGCCACTTGGGAAAAAGATTGAAATCTGCCT
TTTATAGATTGTAATTAAAGGTCCAGGCTTCTAAGCAACTAAATGTTTGTTCGA
AACAAAGTACTTGTCTGGATGTAGGAGGAAAGGGAGTGATGTCACTGCCATTATGATGCC
TTGAATATAAGACCCACTTGCTATCTCCCTGCACCAGCCAGGAGCCACCCATCCTCCAGC
ACACTGAGCAGCAAGCTGGACACACGGCACACTGATCAAATGGTAAGGGATGGTGGCGA
TGCTCATTCTGGGTCTGCTACTTCTGGCGCTGCTCCTACCCGTGCAGGTTCTTCATTGTT
CCTTTAACAGTATGCCGGAAAGCTACTGCAGCCAAACCAAGCCCTCCAACAGTGCCT
ACAGCCTACAGCCGGTCTCCTGTGGCTTGCTTGCCTTACATCTTACCATTAAGAGG
CAGGTCAAGAAACAGCTACAGTTCTCCAACCCATAACACTAAAACCGAATCCAAATGGTGCCT
AGAAGTTCAATGTGGCAAGGAAAAACCAGGTCTCATCAAATCTACTAATTCACTCCTT
ATTAACAGAGAAACGCTTGAGAGTCTCAAACGGACTCGTTAAAGAGCATCTGAAGGATTT
GACTAGATGATAAATGCCTGTACTCCCAGTACTTGGGAGGCCTAGGCCGGGATCACCTG
AGGTCAAGGAGTTGAGACTAACCTGGCAAAATGGTGAACCCCCATCTGTACTAAAATACA
AATATTGACTGGCGTGGTGGTGAGTGCCTGTGATCCCAGCTACTCAGGTGGCTGAAGCAGG
ACAATCACTGAACTCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCGCGCTACTGCACTCTA
GCCTAGCCTGGCAACAGAGTGAGACTTCGTCTCAAAAAAAAGCCAAGTGCAGTGGCT
CACGCCTGTAATCCGGCACTTGGGAGGCCAGGTGGCGGATCACGAGGTCAAGGAGATCA
AGACCATCCTGGCTAATACAGTGAAACCCGTCTACTAAAATACAAAAATTAGCCGGG
GATGGTGGCAGGCACCTGGAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATAGCGTGAA
CTCAGGAGGCAGCTTGCACTGAGCCGAGATTGCGCTACTGCACTCCAGCCTGGCGACAG
CGCGAGACTCCGTCTCAAAAAAA

FIGURE 33

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48309
><subunit 1 of 1, 67 aa, 1 stop
><MW: 6981, pI: 7.47, NX(S/T): 0
MGKGMVAMLILGLLLALLLPVQSSFVPLTSMPEATAAETTKPSNSALQPTAGLLVVLLAL
LHLYH
```

Signal peptide:

amino acids 15-27

FIGURE 34

GGCGCGCGAGAGCGCGCCAGCCCCGCCGCGATGCCCCGCCGCGCCAGGACGCCCTCCTCCCGCTGCTGGCCCCGGCGGCGCCCTGACTCGCCTGCTGCTGCTGGCCATGGCGCGGGCGCTGGGGCGCCCGGGCCAGGGCGGGCGGGCGACGGCGAGGGACGGACAGGACCCGCACAGCAAGCACC TGTACACGGCGACATGTTACGCACGGGATCCAGAGCGCCGCACACTCGTCATGTTCTCGCGCCCTGGTGTG GACACTGCCAGCGGTGCAAGCCACTTGAATGACCTGGAGACAAATACAACAGCATGGAAGATGCCAAAGTCT ATGTGGCTAAAGTGGACTGCACGGCCACTCGACGTGTGCTCGCCAGGGGTGCGAGGATAACCCACCTAA AGCTTTCAAGCCAGGCCAAGAAGCTGTGAAGTACCAAGGGTCTCGGGACTTCCAGACACTGAAAAGTGGATGC TGCAGACACTGAACAGGAGGCCAGTGACACCAGAGCCGAAGTGGAAACGCCAGTGCCTGGAGCTCAAGCAAG GGCTGTATGAGCTCTCAGCAAGCAACTTGAGCTGCACGTTGCAAGGCACCACTTATCAAGTTCTCGCTC CGTGGTGTGGTCACTGCAAAGCCCTGGCTCCAACCTGGAGCAGCTGGCTCTGGCCTTGAACATTCCGAAACTG TCAAGATTGGCAAGGTTGATTGTACACAGCACTATGAACTCTGCTCCGAAACCAGGTTCGTGGCTATCCACTC TTCTCTGGTTCGAGATGGAAAAGGTTGATCAGTACAAGGAAAGCAGGGATTGGAGTCAGTGAGGGAGTACG TGGAGTCGCAGCTGCAGCGCACAGAGACTGGAGCGACGGAGACCGTCACGCCCTCAGAGGCCCGGTGCTGGCAG CTGAGCCCGAGGCTGACAAGGGCACTGTGTTGGCACTCACTGAAAATAACTTGTGATGACACCATTGCAGAAAGGAA TAACCTTCATCAAGTTTATGCTCCATGGTGTGGTCAATTGTAAGACTCTGGCTCCTACTTGGAGGAACACTCTTA AAAAGGAATTCCCTGGTCTGGGGGGTCAAGATGCCGAAGTAGACTGCTGAACGGAAATATCTGCAGCA AGTATTGGTACGGGCTACCCACGTTATTGCTTCCAGGAGGAAGAAAGTCAAGTGGAGGTACAGTGAGCACAGTGGAGGCA GAGACCTTGACTCGTTACACCGCTTGTGCTGAGCCAAGCGAAAGCAGAACCTTAGGAACACAGTGGAGGTAC CTCCTGCCCAGCTCCGCACCCCTGCCTTAGGAGTTCACTGTTCCAGGAGGCCACTGGGTTCCAGTGGTGGCT GTTCAGAAAGCAGAACATACTAAGCGTGAGGTATCTTCTTGTGTTGTTTCAAGGCAACACACTCTACAG ATTCTTATTAAGTTAAGTTCTCAAGTAAATGTGTAACTCATGGTCACTGTGAAACATTTCAGTGGCGATA TATCCCCTTGACCTCTTGTGATGAAATTACATGGTTCTTGAGACTAAATAGCAGTGGAGGAATGAAA TTGCTGGACTATTGTGGCTCTGAGTTGAGTGATTTGGTGAAGAAAGCAGACATCAAAGCATAGTTACCTGC CCACAGGTTCTGAAAGGTGGCTTGTGGCAGTATTGACGTTCTGATCTTAAGGTACAGTGAACACTCAATAC TGTGTTGGTCCGTAGCATGGAGCAGATTGAAATGAAAAACCCACACCTCTGGAAGATACTTCACGGCCGCTGC TGGAGCTCTGTTGCTGTAAGGGCCCTAAGTAGAGTTAGAGTTAGCCGTGATGAAAGCAGCGTTACTTCTGACC GTGCCTGAGTAAGAGAATGCTGATGCCATAACTTATGTGTCGATACTTGTCAAATCAGTTACTGTTAGGGGAT CCTCTGTTCTCACGGGGTGAACATGTCTTGTGTTGAGTCAACACGAAGGCCAGAGCCCACATGAACACTGT TGGATGTTCTCCTAGAAAGGGTAGGCATGGAAAATTCCACGAGGCTCATTCTCAGTATCTCATTAACCTATTGA AAGATTCCAGTTGTATTGTCACCTGGGGTGAACAGACCAGACAGGCTTCCAGGCCTGGGTATCCAGGGAGGC TCTGCAGCCCTGCTGTAAGGGCCCTAAGTAGAGTTAGAGTTCTGATCTGTTCTCAGTAGTCCCTTAGAGG CTTGCTATAACTTGGTCTGCTCAAGGAGGTGCGACCTCTAATGTTGAGAAGAATGGGATGCAATTGATCTCAAGAC CAAAGACAGATGTCAGTGGCTGCTGCCCCGGCTGTGCAACGGCTGTGGCAGCTGTTGATGCCAGTGTCCCTA ACTCATGCTGCTGCTTGTGATTAACACCTCTATCTCCCTGGGAATAAGCACACATACAGGCTTAAGCTCTAAAGATA GATAGGTGTTGTTGCTCTTACCATGAGCTACTTCCCTAATAAACCAACTTGTGATCCAAACACTCTCACCCACCT CCCATACGCAAGGGGATGTGGATACTTGGCCAAAGTAACTGGTGGTAGGAATCTTAGAAACAAAGACCACCTATA CTGTCGAGGAGAAGATAACAGCAGCATCTGACCCAGCCTCTGCCTTAAAGGAAATCTTATTAACTCAG TATGGTTACAGATAATTCTTTTAAAGGAAACCTCTAGAGAAGCACAACACTGTCAGAGTCTGTACA CACAACCTCAGCTTGCATCACGAGTCTGTATTCCAAGAAAATCAAAGGGTACAATTGTTGTTACACTAT GATACTTCTAAATAACTCTTTTTAA

FIGURE 35

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47629, pI: 5.90, NX(S/T): 0
MPARPGRLLPLLARPAALTALLLLGHGGGRWGARAQEAAAAADGPPAADGEDGQDPHS
KHLYTADMFTHGIQSAAHFVMFFAPWCGHCQRLQPTWNDLGDKYNSMEDAKVYVAKVDCTAH
SDVCSAQGVRYGPTLKLKPGQEAVKYQGPRDFQTLENWMLQTLNEEPVTPEPEVEPPSAPE
LKQGLYELSASNFEHVVAQGDHFIKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCT
QHYELCSGNQVRYGPTLLWFRDGKKVDQYKGKRDLESLEYVESQLQRTEGATETVTPSEA
PVLAEEPEADKGTVLALTEENNFDTIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLA
GVKIAEVVDCTAERNICSKYSVRGYPTLLLFRGGKKVSEHSGGRDLDLHRFVLSQAKDEL
```

Signal sequence:

amino acids 1-32

FIGURE 36

CTTTCTGAGGAACCACAGCAATGAATGGCTTGCATCCTGCTTCGAAGAAACCAATTAT
CCTCCTGGTACTATTCTTTGCAAATTCAAGCTGGGTCTGGATATTGATAGCCGTCTA
CCGCTGAAGTCTGTGCCACACACACAATTCAACCAGGACCCAAAGGAGATGATGGTAAAAA
GGAGATCCAGGAGAAGAGGGAAAGCATGGCAAAGTGGACGCATGGGCCGAAAGGAATTAA
AGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCATTGGAAGA
AGGGTACAAAGGGAAAAGGTTGCTTGAATACCTGGAGAAAAGGCAAAGCAGGTACT
GTCTGTGATTGTGGAAGATAACCGAAATTGTTGACAACACTGGATATTAGTATTGCTCGGCT
CAAGACATCTATGAAGTGTCAAGAATGTGATAGCAGGGATTAGGGAAACTGAAGAGAAAT
TCTACTACATCGTCAGGAAGAGAAGAACTACAGGGAACTCCCTAACCCACTGCAGGATTGCG
GGTGAATGCTAGCCATGCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGC
CAAGAGTGGCTTCTCGGGTGTTCATTGGCGTGAATGACCTGAAAGGGAGGGACAGTACA
TGTCCACAGACAAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAACCCAGCGAC
CCCTATGGTCATGAGGACTGTGTGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG
CCATCTTACCATGTACTTGTCTGTGAGTTCATCAAGAAGAAAAGTAACTTCCCTCATCCT
ACGTATTGCTATTCCTGTGACCGTCATTACAGTTATTGTTATCCATCCTTTTCTG
ATTGTACTACATTTGATCTGAGTCACATAGCTAGAAAATGCTAAACTGAGGTATGGAGCCT
CCATCATCAAAAAAAAAAAAAAA

FIGURE 37

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980
><subunit 1 of 1, 277 aa, 1 stop
><MW: 30645, pI: 7.47, NX(S/T): 2
MNGFASLLRRNQFILLVLFLLQIQSLGLDIDSRTAECATHTISPGPKGDDGEKGDPGEEG
KHGKVGRMGPKGIKGELGDMGDQGNIGKTGPIGKKGDKGEKGLLGIPGEKGKAGTVCDGRY
RKFVGQLDISIARLKTSMKFVKNVIAGIRETEEKFYYIVQEEKNYRESLTHCRIRGGMLAMP
KDEAANTLIADYVAKSGFFRVFIGVNDLREGQYMSTDNTPLQNYSNWNEGEPSDPYGHEDC
VEMLSSGRWNDTECHLTMYFVCEFIKKKK
```

Signal peptide:

amino acids 1-25

2
19
18
17
16
15
14
13
12
11
10
9
8
7
6
5
4
3
2
1

FIGURE 38

GGTTCTATCGATTGAATTGGCCACACTGGCCGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACCGCGTCGCTGCTCCGCCGTGGAGTGGTGGGGCTGGGTGGGA**ATGGCGTGT**
GCCAGCGCACCGCGCTCCCTGGAAAGGAGAAGTCTCAGCTAGAACCGAGCGGCCCTAGGTTT
CGGAAGGGAGGATCAGGGATGTTGCGAGCGGCTGGAACCCAGACGGTCCGATAGAGGAAGC
GGGCTCCATGGCTGCCCTCGCTGCTGCCCTGCTGCTGTTGCTACCGCTGCTGCTGA
AGCTACACCTCTGGCCGAGTTGCGCTGGCTTCCGGGACTTGGCTTTCGGGTGCGAGCT
CTGTGCTGAAAAGGGCTTTCGAGCTCGGCCCTGGCCGGCTGCCGCCACCGGAAGG
TCCCAGGGGGCTGCAGCCTGGCCTGGCGCTCGCGGAACCTGGCCAGCAGCGCGCCGCG
ACACCTTCTCATTACGGCTCGGGCGCTTAGCTACTCAGAGGCGAGCGAGAGTAAC
AGGGCTGCACCGCCTCCTACGTGCGCTAGGCTGGACTGGGACCCGACGGCGGACAG
CGCGAGGGAGCGCTGGAGAAGGCGAGCGGGCAGCGCCGGAGCCGGAGATGCAGCGGCCG
GAAGCGCGCGGGAGTTGCCGGAGGGACGGTGCCCGAGAGGTGGAGGAGCCGCCCG
CTGTCACCTGGAGCAACTGTGGCGCTGCTCCTCCCCGCTGGCCAGAGTTCTGTGGCTCTG
GTTCGGGCTGGCAAGGCCGGCTGCGCACTGCCCTTGTGCCAACGCCCTGCGCCGGGCC
CCCTGCTGCAC TGCTCCGAGCTGCGCGCGCGCTGGTGCCTGGCGCAGAGTTCTG
GAGTCCCTGGAGCCGGACCTGCCCGCTGAGAGCCATGGGCTCCACCTGTGGCTGCAGG
CCCAGGAACCCACCTGTTAGCGATTGCTGGCTGAAGTGTCCGCTGAAGTGGATG
GGCCAGTGCAGGATACCTCTCTTCCCCCAGAGCATAACAGACACGTGCCTGTACATCTC
ACCTCTGGCACCAAGGGCTCCCCAAGGCTGCTGGATCAGTCATCTGAAGATCCTGCAATG
CCAGGGCTTCTATCAGCTGTGGTGTCCACCAGGAAGATGTGATCTACCTGCCCTCCCAC
TCTACCACATGTCCGGTCCCTGCTGGCATCGTGGGCTGCATGGCATTGGGCCACAGTG
GTGCTGAAATCCAAGTTCTCGGCTGGTCAAGTTCTGGGAAGATTGCCAGCAGCACAGGTGAC
GGTGTCCAGTACATTGGGAGCTGTGCCGATACCTGTCAACCAGCCCCGAGCAAGGCAG
AACGTGGCCATAAGGTCCGGCTGGCAGTGGCAGCGGGCTGCCACAGATACTGGAGCGT
TTTGTGGCGCTCGGGCCCTGCAGGTGCTGGAGACATATGGACTGACAGAGGGCAACGT
GCCACCATCAACTACACAGGACAGCGGGCGCTGTGGGCGTCTGGCTTACAAGC
ATATCTCCCTCTCCTGATTGCTATGATGTCACCACAGGAGAGCCAATTGGGACCCC
CAGGGCACTGTATGCCACATCTCAGGTGAGCCAGGGCTGCTGGCCCGTAAGCCA
GCAGTCCCCATTCTGGCTATGCTGGCCAGAGCTGGCCACAGGGGAAGTTGCTAAAGG
ATGTCTCCGGCTGGGATGTTCTTCAACACTGGGACCTGCTGGTCTGCGATGACCAA
GGTTTCTCGCTTCCATGATCGTACTGGAGACACCTCAGGTGGAAGGGGAGAATGTGGC
CACAACCGAGGTGGCAGAGGTCTCGAGGCCCTAGATTTCTTCAGGAGGTGAACGTCTATG
GAGTCAGTGTGCCAGGGCATGAAGGCAGGGCTGGAATGGCAGGCCCTAGTCTCGTCCCCC
CACGCTTGGACCTTATGCAGCTCTACACCCACGTGCTGAGAACCTGCCACCTTATGCCG
GCCCGATTCTCAGGCTCCAGGAGTCTTGGCCACCACAGAGACCTCAAACAGCAGAAAG
TTCGGATGGCAAATGAGGGCTCGACCCAGCACCTGCTGACCCACTGTACGTTCTGGAC
CAGGCTGTAGGTGCCTACCTGCCCTCACAACTGCCGGTACAGGCCCTCTGGCAGGAAA
CCTTCGAATCT**GA**AACTTCCACACCTGAGGCACCTGAGAGAGGAACCTGTGGGGGG
CCGTTGCAGGTGTACTGGGCTGTCAGGGATCTTCTATACAGAACCTGCGGTCACTATT
GTAATAAAATGTGGCTGGAGCTGATCCAGCTGTCTGACCTAAAAAAAAAAAAAAA
AAAAAAAAGGGCGGCCGACTCTAGAGTCGACCTGCAAGTAGGGATAACAGGGTAATAAGC
TTGGCCGCCATGGCCAACCTGTTATTGCAG

FIGURE 39

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50913
><subunit 1 of 1, 730 aa, 1 stop
><MW: 78644, pI: 7.65, NX(S/T): 2
MGVCQRTRAPWKEKSQLEAALGFRKGSGMFASGWNQTVPIEEAGSMAALLLPLLLLPL
LLLKLHLWPQLRWLPADLAFAVRALCCKRALRALARAAAAADPEGPEGGCSLAWRLAELAQ
RAAHTFLIHGSRRFSYSEAERESNRAARAFLRALGWDWGPDGGSGEGSAGEGERAAPGAGD
AAAGSGAEFAGGDGAARGGAAAPLSPGATVALLPAGPEFLWLWFGGLAKAGLRTAFVPTAL
RRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSA
EVDGPVPGYLSSPQSIIDTCLYIFTSGTTGLPKAARIHLKILQCQGFYQLCGVHQEDVIYL
ALPLYHMSGSLGIVGCMGIGATVVLKSFKSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPP
SKAERGHKVRLAVGSLRPDTWERFVRRGPLQVLETYGLTEGNVATINYTGQRGAVGRASW
LYKHIFPFSLIRYDVTGEPIRDQGHCMATSPGEPGLVAPVSQQSPFLGYAGGPелаQGK
LLKDVFRPGDVFFNTGDLLVCDDQGFLRFHDRTGDTFRWKGENVATTEVAEVFEALDFLQEV
NVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPYARPRFLRLQESLATTETFK
QQKVRMANEGFDPSTLSDPLYVLDQAVGAYLPLTTARYSALLAGNLRI
```

Type II transmembrane domain:

amino acids 45-65

Other transmembrane domain:

amino acids 379-398

cAMP- and cGMP-dependent protein kinase phosphorylation site

starting at amino acid 136

CUB domain protein motif

amino acids 254-261

putative AMP-binding domain signature

amino acids 332-343

N-glycosylation sites

amino acids 37-40 and 483-486

FIGURE 40

CCTGTGTTAAGCTGAGGTTCCCTAGATCTGTATATCCCCAACACATACTCCACGCACA
CACATCCCCAAGAACCTCGAGCTCACACCAACAGACACACCGCGCAGCTACACACTCGCTCTC
GCTTGTCCATCTCCCTCCGGGGAGCCGGCGCGCTCCACCTTGCCGCACACTCCGGC
GAGCCGAGCCCGCAGCGCTCCAGGATTCTCGGCGCTCGGAACCTGGATTGCAGCTCTGAACCC
CCATGGTGGTTTTAACACTTCTTTCTCTCTTCCTCGTTGATTGCACCGTTCCA
TCTGGGGCTAGAGGAGCAAGGCAGCAGCCTCCAGCCAGCCCTGTTGGCTGCCATCGT
CCATCTGGCTTATAAAAGTTGCTGAGCGCAGTCAGAGGGCTGCCTGCTCGTCCCCTCGG
CTGGCAGAAGGGGTGACGCTGGCGAGCGCGAGGAGCGCGCCCTGCCTCTGGCGGGCTTT
CGGCTTGAGGGCAAGGTGAAGAGCGCACCGCCGTGGGTTACCGAGCTGGATTGTATG
TTGCACCA**ATG**CCTCTTGGATCGGGCTGTGATTCTTCCCTTTGGGCTGCTGCTCTCCC
TCCCCGCCGGGGCGGATGTGAAGGCTCGAGCTCGGAGAGGTCCGCCAGGCAGGGTGC
AAGGGATTCAAGCTGGCGGACATCCCCTACCAAGGAGATCGCAGGGAAACACTTAAGAATCTG
TCCTCAGGAATATACATGCTGCACCACAGAAATGGAAGACAAGTTAAGCCAACAAAGCAAAC
TCGAATTGAAAACCTTGTGGAAGAGACAAGCCATTGTCGCACCACTTTGTGTCAGG
CATAAGAAATTGACGAATTTCGAGAGCTCTGGAGAATGCAAGAAAAGTCACAAATGA
TATGTTGTACGGACCTATGGCATGCTGTACATGCAATTAGAAGTCTTCAGGACCTCT
TCACAGAGCTGAAAGGTACTACACTGGGGTAATGTGAATCTGGAGGAATGCTCAATGAC
TTTGGGCTCGCTCTGGAACGGATGTTCAGCTGATAAAACCTCAGTATCACTTCAGTGA
AGACTACCTGGAATGTGTGAGCAAATACACTGACCAAGCTCAAGCCATTGGAGACGTGCC
GGAAACTGAAGATTCAAGGTTACCCGCGCCTTCATTGCTGCCAGGACCTTGCCAGGGCTG
ACTGTGGCAGAGAAGTTGCAAACCGAGTTCCAAGGTCAAGCCAACCCCAGGTGTATCCG
TGCCCTCATGAAGATGCTGTACTGCCATACTGTCGGGGCTTCCACTGTCAGGCC
ACAACACTGTCACGTCATGAAGGGCTGTTGGCAAATCAGGCTGACCTCGACACAGAG
TGGAAATCTGTTATAGATGCAATGCTCTGGTGGCAGAGCGACTGGAGGGCCATTCAACAT
TGAGTCGGTCACTGGACCCGATAGATGTCAGATTCTGAAGCCATTATGAACATGCAAGAAA
ACAGCATGCAGGTGTCAGTCAAAGGTCTTCAGGGATGTGGTCAGCCAAACCTGCTCCAGCC
CTCAGATCTGCCGCTCAGCTCTGAAATTAAACACGTTCAAGGCCACAATCCTGA
GGAAAGACCAACAACGTCAGGCACAAGCTGGACCGCTGGTCACAGACATAAAAGAGA
AATTGAAGCTCTAAAGGTCTGGTCAGCATTACCTACACTATGTCAGGACGAGAG
GTGACAGCGGGCACGTCAAACGAGGAGGAATGTCAGGACAGCAAAGCCAGATACTT
GCCTGAGATCATGAATGATGGGCTCACCAACCAGATCAACAATCCGAGGTGGATGTGGACA
TCACTCGGCTGACACTTCATCAGACAGCAGATTATGGCTCTCCGTGTGATGACCAACAAA
CTAAAAAAACGCTTACAATGGCAATGATGTCAGATTCCAGGACACAAGTGTGATGAATCCAGTGG
CTCAGGGAGTGGCAGTGGTGCATGGATGACGTGTGTCAGGAGTTGAGTTGTCACCA
CAGAGGCCCGCAGTGGATCCCGACCGGAGAGAGGTGGACTCTCTGCAGCCCAGCGTGGC
CACTCCCTGCTCTGGTCTCAGATGCAATTGTCAGGACAGAAACTGCTGTCAGAGACTGTGCA
GA
ATCTTGGGTTTGTCAGATGAAACTGCATTAGCTATGTCAGGACACTCACTTCTT
TTCTTACACTCTGGACAATGGACCATGCCACAAAAACTTACCGTTCTATGAGAAGAGAG
CAGTAATGCAATCTGCCTCCCTTTGTTCCAAAGAGTACCGGGTGCCAGACTGAAC
CTTCCTCTTCAGCTATGTCAGGAGCTTGTGTTATTCTAGAGAGAATTCTTACTCAA
ATTTTCGTACCAAGGAGATTCTTACCTCATTGCTTTATGTCAGAAGTAAAGGAAT
CTCACGTTGTGAGGGTTTTTTCTCATTAAAAT

FIGURE 41

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914
><subunit 1 of 1, 555 aa, 1 stop
><MW: 62736, pI: 5.36, NX(S/T): 0
MPSWIGAVILPLLGLLSSLPAGADVAKARSCGEVRQAYGAKGFSLADI PYQEIA GEHLRICPQ
EYTCCTTEMEDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLENAEKS LNDMF
VRTYGM LYMQNSEVFQDLFTELKRYYTGGNVNLEEMLNDFWARLLERMFQLINPQYHFSEDY
LECVSKYTDQLKPFGDVPRKLKIQVTRA FIAARTFVQGLTVGREVANRVSKVSPTPGCIRAL
MKMLYCPYCRGLPTVRPCNNYCLNV MKGCLANQADLDTEWNLFIDAMLLVAERLEGPFNIES
VMDPIDVKISEAIMNMQENSMQVSAKVFQGCGQPKPAPALRSARSAPENFNTRFRPYNPEER
PTTAAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDESVTAGTSNEEECWNGHSKARYLPE
IMNDGLTNQINNPEVDVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSG
SGSGCMDDVCPTEFVTEAPAVDPDRREVDSSAAQRGHSSLWSLTCIVLALQRLCR
```

Signal peptide:

amino acids 1-23

FIGURE 42A

CGGACGCGTGGCGGACGCGTGGCAAAGAACTCGGAGTGCCAAGCTAAATAAGTTAGCTGAGAAAACGCACG
CAGTTGCAGCGCTGCGCCGGTGCGCCAACCTACGCAAAGACCAAGCGGGCTCCGCGCGACCGGCCGGGGC
TAGGGACCCGGCTTGGCCTTCAGGCTCCCTAGCAGCGGGAAAAGGAATTGCTGCCGGAGTTCTCGGGAGGT
GGAGGGAGATCAGGAAACGGCTTCTCCTCACTTCGCCCTGGTAGTGAGTGTGGAGATTGGCAAACGCCTAGG
AAAGGACTGGGAAAATAGCCCTGGAAAGTGGAGAAGGTGATCAGGAGGCCGGTCCACTACGGCAGTTATCTG
TCTGATCAGAGCCAGCGACGCGTCCACTTCGAGTTCTTCAGGTGTGGGACCGCAGGACAGACGCCGA
TCCCGCCGCCCTCCGTACCAGCACTCCAGGAGAGTCAGCCTCGCTCCCAACGTCGAGGGCGCTGGCACGA
AAAGTTCTGTCCACTGTGATTCTCAATTCTTGTGGTTTTCTCCAGAGAACTTTGGGTGGAGATATTA
ACTTTTTCTTTTTTTCTTGGTAGCTGCTCTAGGGAGGGGGAGGAGGAGGAGAAAGTGAATGTGC
TGGAGAAGAGCGAGCCCTCCTGTTCTCCGGAGTCCCATTAGGCATCACCTCTGGAAGATTAAAGTTGT
CGGACATGGTACAGCTGAGAGGAGAGGAGGATTCTTGCCAGGTGGAGAGTCCTCACCGTCTGGTGCATG
TGTGCGCCCGCAGCGCGCGGGCGCTGGTCTCCGCGTGGAGTCACCTGGGACCTGAGTGAATGGCTCCA
GGGGCTGTGCGGGCATCCGCCCTCCGCTTCTCCACAGGCCTGTGTCTGCTGGAAAGATGCTAGCAATGGGG
CGCTGGCAGGATTCTGGATCCTCTGCCCTCCTACTTATGGTACCTGTCCTGGGCCAGGCCTAGAAGAGGAGG
AAGAAGGGGCCTACTAGCTAACGCTGGAGAGAAACTAGAGGCCAGCACAACTTCCACCTCCAGCCCCATCTCA
TTTCATCCTAGCGGATGATCAGGGATTAGAGATGTGGTTACCACGGATCTGAGATTAAAACACCTACTCTG
ACAAGCTCGCTGCCGAAGGAGTTAAACTGGAGAACTACTATGTCCAGCCTATTGACACCCATCCAGGAGTCAGT
TTATTACTGAAAGTATCAGATAACACACCGACTTCAACATTCTATCATAAGACCTACCCAAACCAACTGTTAC
CTCTGGACAATGCCACCTACCTCAGAAACTGAAGGAGTTGGATATTCAACGCATATGGTGGAAAATGGCACT
TGGGTTTTAACAGAAAAGATGCATGCCACCAGAGAGGAGTTGATACTTTGGTCCCTTTGGGAAGTG
GGGATTACTATACACACTACAAATGTGACAGTCCTGGATGTGTGGCTATGACTTGTATGAAAACGACAATGCTG
CCTGGGACTATGACAATGGCATATACTCCACACAGATGTACACTCAGAGAGTACAGCAAATCTAGCTCCATA
ACCCCAACAAAGCCTATATTTTATATACTGCCTATCAAGCTGTTCACTCAGACTGCAAGCTCCTGGCAGGTATT
TCGAACACTACCGATCCATTATCAACATAAACAGGAGAAGATATGCTGCCATGCTTCTGCTTAGATGAAGCAA
TCAACAAACGTGACATTGGCTCTAAAGACTTATGGTTCTATAACAAACAGCATTATCATTACTCTCAGATAATG
GTGGCCAGCCTACGGCAGGAGGGAGTAACGGCCTCTCAGAGGTAGCAAAGGAACATATTGGGAAGGAGGGATCC
GGGCTGTAGGTTGTGCATAGCCACTTCTGAAAACAAGGGAACAGTGTGTAAGGAACATTGTGCACATCACTG
ACTGGTACCCACTCTCATTCACTGGCTGAAGGACAGATTGATGAGGACATTCAACTAGATGGCTATGATATCT
GGGAGACCATAAAGTGGGCTTCAGGCTACCCCGAGTAGATATTGACATACCTGACCCATACACCAAGGC
AAAAAAATGGCTCTGGCAGCAGGCTATGGGATCTGGAACACTGCAATCCAGTCAGCCATCAGAGTGCAGCACTG
GAAATTGCTTACAGGAAATCTGGCTACAGCGACTGGTCCCCCTCAGTCTTCAGCAACCTGGACCGAACCG
GTGGCACAATGAACGGATCACCTGTCAACTGGCAAAGTGTATGGTTCAACATCACAGCCGACCCATATGA
GAGGGTGGACCTATCTAACAGGTATCCAGGAATCGTGAAGAAGCTCCTACGGAGGCTCTCAGTTCAACAAAAC
TGCAGTGCCGGTCAGGTATCCCCCCTAAAGACCCAGAGTAACCTAGGCTCAATGGAGGGCTGGGACCATG
GTATAAAAGAGGAAACCAAGAAAAGAAGCCAAGCAAAATCAGGCTGAGAAAAGCAAAGAAAAGCAAAAAAAA
GAAGAAGAAACAGCAGAAAGCAGTCTCAGGTAAACCAGCAAATTGGCTCGATAATATCGCTGGCTAACGCTCA
GGCTTGTGTTCATGCTGTGCCACTCCAGAGACTTCTGCCACCTGGCCACACTGAAAATGTCTGCTCAGTG
CCAAGGTGCTACTCTGCAAGCCACACTTAGAGAGAGTGGAGATGTTATTCTCGCTCCTTAGAAAACGTG
GTGAGTCTGAGTCCACTGCTGTGCTTCAGTCAACTGACCAAACACTGCTTGAATTATAGGAGGAGAACATA
ACCTACCACCGCAAGCATGCTAATTGATGGAAGTTACAGGGTAGCATGATTAAACTACCTTGATAAATTAC

FIGURE 42B

AGTCAAAGATTGTGTCACCTCAAAGGCCTTGAAGAATATATTTCTTGGTGAATTTTGTATGTCTGTATATGA
CACTTGGGTTTTAATTAAATTCTATTATATATAAATATGTTCTTCTGTGAAAAGCTTTCT
CACATGTGAACAGCTTGCACCTCATTACCATGCGTAGGGAAATGGCAAATAAGAATGTTGAGCACACTGCC
ACAATGAATGTAACATTTCTAACACTTACTAGAAGAACATTCAGTATAAAAAACCTAATTATTTACA
GAAAATATTTGTTGTTTATAAAAAGTTATGCAAATGACTTTATTTTATTCCTGCATACCATAGAAGA
ATTTTATTCATTCTCAAATTATCAAGCACTGTAATACTATAAATTAAATGTAATACTGTGTAATTCA
TAAAAAACATCATTCAAGAAACTTATAATCGTCAATTGTTCAATCAAGATTTGAATGTAATAAGATGAATATAT
ATTACTTGGAAATTCAATGTTGTCAGAGTTGAGACAACCTTATTGTTCTATCATAAAACTATTTATGTATCTT
AATTATTAAAATGATTACTTATGGCACTAGAAAATTACTGTGGCTTTCTGATCTAACCTCTAGCTAAAATT
GTATCATTGGCCTAAAAATAAAACTTTACTAATAGGCATTGAGGAATGGTTGCTAACACCACAGTAA
TATAATATGATTACAGATAGATGCTCCCCCTGGCTATGACATGGAGAAAGATTTCCATAATAAACTAA
TATTTATATTAGGTTGGCAAAACTAGTTGCGGTTTCCATTAAAAGTAATAACCTTACTCTTACAAAGT
GGACACTGTGGGAGATAAGAGAAATGGAAGATAACGGATCCTGCCTGGAGTAGGTAACCTGCTGGAAACCCC
ACATGCAAACGTCAATGAGGAGAATTAAAGGAGTATTACAGTAATGAAGTTATCATGGGTCAATGAGCATA
GATTGGTGTGGATCCTGTAGACCCCTGGTGTTCCTTGAAGTGCCCTCTCCTAATGCAGAGGCCTGAGCTTAC
AGTATACACTTGAAAAGTCACAGATAGCTAGAATTATGATCTTGAAGTTATAACTGTGATCTGAAAATGTGT
GGTGGTATGACAGCATACCATTAAATACATTACATCACAGCTCAAAGGACTGTGATATAATCCATTATAC
AACTCAAAGGACTGTGATATAATCCATTATACAGCTCACAGTTCTGAAAATGTATAAAAGAATCTATAAT
CTAGTACTGAAATTACTAAATTGGTAAGATGATTAAATGATTAAATTAAACATTATTTCTAGAATATAT
GGCTCCATTATTTATAGTGTAAAGTTGTATTCTCTAAAGTTGTGTTGTCGACAGTATCTTAAATGAG
TCTTAAAAATAAGGCATATTGTCATGTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AA

FIGURE 43

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296
><subunit 1 of 1, 515 aa, 1 stop
><MW: 56885, pI: 6.49, NX(S/T): 5
MAPRGCAHGPPPSPQACVCPGKMLAMGALAGFWILCLLTGYLSWGQALEEEEGLAQA
GEKLEPSTTSTSQPHLIFILADDQGFRDVGYHGSEIKTPTLDKLAEGVKLENYYVQPICTP
SRSQFITGKYQIHTGLQHSIIRPTQPNCLPLDNATLPQKLKEVGYSTHMVGKWHLGFRKEC
MPTRRGFDTFFGSLLGSGDYYTHYKCDSPGMCGYDLYENDNAAWDYDNGIYSTQMYTQRVQQ
ILASHNPTKPIFLYTAQAVHSPLQAPGRYFEHYRSIININRRRYAAMSLDEAINNVTLA
LKTYGFYNNNSIIYSSDNGQPTAGGSNWPLRGSKGTWEGGIRAVGFVHSPLLKNKGTVCK
ELVHITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPG
QQAMGSGTLQSSQPSECSTGNCLQEILATATGSPLSLSATWDRTGGTMNGSPCQLAKVYGF
TSQPTHMRGWTYLTGIQES
```

Important Features:

Signal Peptide:

amino acids 1-37

Sulfatases signature 1.

amino acids 120-132

Sulfatases signature 2.

amino acids 168-177

Tyrosine kinase phosphorylation site.

amino acids 163-169

N-glycosylation sites.

amino acids 157-160, 306-309 and 318-321

FIGURE 44

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCGAGCGGCTGAGGAGAGAGGAGGCGGCGGC
TTAGCTGCTACGGGGTCCGGCGCCCTCCCGAGGGGGCTCAGGAGGAAGGAGGAC
CCGTGCGAGAATGCCTCTGCCCTGGAGCCTGCGCTCCCGCTGCTCTCTGGTGGCAG
GTGGTTCGGGAACCGCGCCAGTGCAAGGCATCACGGGTTGTTAGCATGGCACGTAGCCT
GGGGTCTGTCACTATGGAACTAAACTGGCCTGCTGCTACGGCTGGAGAAGAACAGCAAGGG
AGTCTGTGAAGCTACATGCGAACCTGGATGTAAGTTGGTGAGTGCCTGGGACCAAACAAAT
GCAGATGCTTCCAGGATAACACGGAAAACCTGCAGTCAGATGTGAATGAGTGTGGAATG
AAACCCGGCCATGCCAACACAGATGTGAATACACACCGGAAGCTACAAGTGCTTGCCT
CAGTGGCCACATGCTCATGCCAGATGCTACGTGTGAACTCTAGGACATGTGCCATGATAA
ACTGTCAGTACAGCTGTGAAGACACAGAAGAAGGCCACAGTGCCTGTGCATCCTCAGGA
CTCCGCCTGGCCCCAAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCCTGGTAAAGT
CATCTGTCCCTACAATCGAAGATGTGTGAACACATTGGAAGCTACTACTGCAAATGTCACA
TTGGTTCGAAGTGCATATATCAGTGGACGATATGACTGTATAGATATAATGAATGTACT
ATGGATAGCCATACGTGCAGCCACCATGCCAATTGCTCAATACCCAAAGGGCCTTCAGTG
TAAATGCAAGCAGGGATATAAAGGCAATGGACTTCGGTGTCTGCTATCCCTGAAAATTCTG
TGAAGGAAGTCCTCAGAGCACCTGGTACCATCAAAGACAGAATCAAGAAGTGCTTGCTCAC
AAAAACAGCATGAAAAAGAAGGCAAAATTAAAATGTTACCCAGAACCCACCAGGACTCC
TACCCCTAAGGTGAACCTGCAGCCCTCAACTATGAAGAGATAGTTCCAGAGGCGGGAACT
CTCATGGAGGTAAAAAGGGAATGAAGAGAAATGAAAGAGGGCTTGAGGATGAGAAAAGAG
AAGAGAAAGCCCTGAAGAATGACATAGAGGAGCGAACGCTGCGAGGAGATGTGTTTCCCT
AAGGTGAATGAAGCAGGTGAATTGGCCTGATTCTGGTCAAAGGAAAGCGCTAACTTCAA
ACTGGAACATAAAGATTAAATATCTCGGTTGACTGCAGCTCAATCATGGATCTGTGACT
GGAAAACAGGATAGAGAAGATGATTTGACTGGAATCCTGCTGATCGAGATAATGCTATTGGC
TTCTATATGGCAGTCCGGCCTGGCAGGTACAAGAAAGACATTGGCGATTGAAACTTCT
CCTACCTGACCTGCAACCCAAAGCAACCTCTGTTGCTCTTGATTACCGGCTGGCCGGAG
ACAAAGTCGGAAACTTCGAGTGTGAAAAACAGTAACAATGCCCTGGCATGGGAGAAG
ACCACGAGTGAGGATGAAAAGTGGAAGACAGGGAAAATTCAAGTTGATCAAGGAACTGATGC
TACCAAAAGCATCATTGAAAGCAGAACGTGGCAAGGGAAAACCGGCGAAATCGCAGTGG
ATGGCGTCTTGCTTGTGTTAGGCTTATGTCCAGATAGCCTTTATCTGTGGATGACTGAATG
TTACTATCTTATATTGACTTTGATGTTGATGTCAAGTCCCTGGTTTTTGATATTGCATCATAG
GACCTCTGGCATTAGAATTACTAGCTGAAAATTGTAATGTACCAACAGAAATATTATTG
TAAGATGCCTTCTTGATAAGATATGCCAATATTGCTTAAATATCATATCACTGTATCT
TCTCAGTCATTCTGAATCTTCCNCATTATATTATAAAATNTGAAANGTCAGTTATCTC
CCCTCCTCNGTATATCTGATTGATANGTANGTTGATGNGCTCTCTACAACATTTCTA
GAAAATAGAAAAAAAGCACAGAGAAATGTTAAGTGTGACTCTTATGATACTTCTGG
AACTATGACATCAAAGATAGACTTTGCCTAAGTGGCTTAGCTGGTCTTGTAGCCAAAC
TTGTATATTAAATTCTTGTAATAATAA

FIGURE 45

MPLPWSLALPLLLSWVAGGFNAASARHHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCE
ATCEPGCKFGECVGPNCRCPGTYGKTCQDVNECGMKPRPCQHRCVNTHGSYKCFCLSGH
MLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAPNGRDCLDIDEASGKVICP
YNRRCVNTFGSYYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFTQGSFKCKCK
QGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAHKNSMKKAKIKNVTPERTRPTPK
VNLQPFNYEEIVSRGGNSHGGKGNEEK

Signal peptide:

amino acids 1-21

EGF-like domain cysteine pattern signature.

amino acids 80-91

Calcium-binding EGF-like domains

amino acids 103-124, 230-251 and 185-206

FIGURE 46

GGGAGCTGCTGCTGTGGCTGCTGGTCTGCGCGCTGCTCCTGCTCTGGTGCAGCTGCTG
CGCTTCCTGAGGGCTGACGGCAGCTGACGCTACTATGGGCCGAGTGGCAGGGACGACGCC
AGAATGGGAGCTGACTGATATGGTGGTGTGGTGACTGGAGCCTCGAGTGGATTGGTGAGG
AGCTGGCTTACCAAGTTGTCTAAACTAGGAGTTCTCTTGCTGTCAGCCAGAAGAGTCAT
GAGCTGGAAAGGGTGA
AAAAGAAGATGCCTAGAGAATGGCAATTAAAAGAAAAGATATACT
TGTGTTGCCCTTGACCTGACCGACACTGGTCCCATGAAGCGGCTACCAAAGCTGTTCTCC
AGGAGTTGGTAGAATCGACATTCTGGTCAACAATGGTGAATGTCCCAGCGTTCTGTGC
ATGGATACCAGCTGGATGTCTACAGAAAGCTAATAGAGCTTAACACTTAGGGACGGTGTC
CTTGACAAAATGTGTTCTGCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA
ATAGCATCCTGGGTATCATATCTGTACCTCTTCCATTGGATACTGTGCTAGCAAGCATGCT
CTCCGGGGTTTTTAATGGCCTCGAACAGAACTGCCACATACCCAGGTATAATAGTTTC
TAACATTGCCAGGACCTGCAATCAAATATTGGAGAATTCCCTAGCTGGAGAAAGTCA
CAAAGACTATAGGCAATAATGGAGACCAGTCCCACAAGATGACAACCAGTCGTTGTGCGG
CTGATGTTAACATCAGCATGGCAATGATTGAAAGAAGTTGGATCTCAGAACACCTTCTT
GTTAGTAACATATTGTGGCAATACATGCCAACCTGGCCTGGTGGATAACCAACAAGATGG
GGAAGAAAAGGATTGAGAACTTTAACAGAGTGGTGGATGCAGACTCTCTTATTAAAATC
TTAACAGAAAACATGACTGA
AAAAGAGCACCTGTACTTTCAAGCCACTGGAGGGAGAAATG
GAAAACATGAAAACAGCAATCTCTTATGCTCTGAATAATCAAAGACTAATTGATTT
ACTTTTAATAGATATGACTTGCTTCAACATGGAATGAAATAAAAATAATAAAAAG
ATTGCCATGAATCTTGCAAAA

FIGURE 47

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA36343
><subunit 1 of 1, 289 aa, 1 stop
><MW: 32268, pI: 9.21, NX(S/T): 0
MVVWVTGASSGIGEELAYQLSKLGVLVLSARRVHELERVKRRCLEGNLKEKDILVLPLDL
TDTGSHEAATKAVLQEFGGRIDILVNNGGMSQRSLCMDTSLDVYRKLIELNYLGTVSLTKCVL
PHMIERKQGKIVTVNSILGIISVPLSIGYCASKHALRGFFNGLRTELATYPGIIVSNICPGP
VQSNIVENSLAGEVTKTIGNNGDQSHKMTTSRCVRLMLISMANDLKEVWIEQPFLLVTLW
QYMPTWAWWITNKGKKRIENFKSGVDADSSYFKIFKTKHD
```

Important Features:

Signal Peptide:

amino acids 1-31

Transmembrane domain:

amino acids 136-157

Tyrosine kinase phosphorylation site.

106-113 and 107-114

Homologous region to Short-chain alcohol dehydrogenase

amino acids 80-90, 131-168, 1-13 and 176-185

FIGURE 48

GCGACGTGGGCACCGCCATCAGCTGTTCGCGCGTCTCTCTCCAGGTGGGGCAGGGGTTTC
GGGCTGGTGGAGCATGTGCTGGACAGGACAGCATCCTCAATCAATCAAACAGCATATTGG
TTGCATCTTCTACACACTACAGCTATTGTTAGGTTGCCTCGGACACGCTGGCCTGTCC
TGATGCTGCTGAGCTCCCTGGTGTCTCGCTGGTCTGTACCTGGCCTGGATCTGTTC
TTCGTGCTCTATGATTCTGCATTGTTGTATCACCACCTATGCTATCAACGTGAGCCTGAT
GTGGCTCAGTTCCGGAAGGTCCAAGAACCCCAGGGCAAGGCTAAGAGGCAGTGGCCCTCA
ACCCAAAGCCAGGCTGACCTCATCTGCTTGCTTGGTCTCAAGCCGCTCAGCGTGCCTGTG
GACAGCGTGGCCCCGGCCCCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCCC
TGGCAGGCCAGTGTGAGGAGGCAAGGAGCCCACATCTGCAGCGGCTCCCTGGTGGCAGACAC
CTGGGTCTCACTGCTGCCACTGCTTGTAAAAGGCAGCAGCAACAGAACTGAATTCTGGT
CAGTGGTCTGGGTTCTGCAAGCGTGGAGGACTCAGCCCTGGGCGAAGAGGTGGGGTG
GCTGCCCTGCAGTTGCCAGGGCTATAACCACTACAGCCAGGGCTCAGACCTGGCCCTGCT
GCAGCTCGCCCACCCACGACCCACACACCCCTCTGCCTGCCAGCCCAGCCATCGCTTCC
CCTTGAGGCTCCTGCTGGCCACTGGCTGGATCAGGACACCAAGTGTGCTCTGGGACC
CTACGCAATCTGCGCCTGCGTCTCATCAGCGCCACATGTAAGTGTATCTACAACAGCT
GCACCAGCGACACCTGTCACCCGGCCCTGGGATGCTATGTGGGGGCCAGCCTG
GGGTGCAGGGCCCTGTCAGGGAGATTCCGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGA
CACTGGGTTCAGGCTGGCATCATCAGCTTGATCAAGCTGTGCCAGGAGGACGCTCTGT
GCTGCTGACCAACACAGCTGTCACAGTTCTGGCTGCAGGCTCGAGTTCAAGGGCAGCTT
TCCTGGCCAGAGCCAGAGACCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGA
TCCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCCCTCCCATGGCCCTGGGAGGCCAGGCT
GATGCACCAGGGACAGCTGGCTGTGGCGAGCCCTGGTGTAGAGGAGGCCGGTCTAACTG
CTGCCCACTGCTTCATTGGGCGCCAGGCCAGAGGAATGGAGCGTAGGGCTGGGACCAGA
CCGGAGGAGTGGGGCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCCTGAGGGGG
CTACGACATGGCCCTCCTGCTGGCCAGCCTGTGACACTGGGAGGCCAGCCTGCAGGCC
TCTGCCTGCCCTATCCTGACCACACCTGCCTGATGGGAGCGTGGCTGGTTCTGGGACGG
GCCCGCCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCAGCCTCTGGGCC
GGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGTGTGGCAGCCCTATTCTGCCGGGATGG
TGTGTACCACTGCTGTGGGTGAGCTGCCAGCTGTGAGGGCTGTCTGGGACCAACTGGT
CATGAGGTGAGGGCACATGGTTCTGGCCGGCTGCACAGCTCGAGATGCTTGCAGG
CCCCGCCAGGCCGGCTTCAACCGCGCTCCCTGCCTATGAGGACTGGGTAGCAGTTGG
ACTGGCAGGTCTACTTCGCCAGGAACCAGAGCCGAGGCTGAGCCTGGAAAGCTGCC
AACATAAGCCAACCAACCAGCTG**TGA**CAGGGACCTGGCATTCTCAGGACAAGAGAAATGC
AGGCAGGCAAATGGCATTACTGCCCTGTCCCTCCCCACCCCTGTGATGTGTGATTCCAGGCAC
CAGGGCAGGCCAGAACGCCAGCAGCTGTGGAGGAACCTGCCTGGGCCACAGGTGCC
CTCCCCACCCCTGCAGGACAGGGGTGTCTGTGGACACTCCCACACCCAACTCTGCTACCAAGC
AGGCCTCTCAGCTTCTCCTCCTTACTCTTCAGATAACAATCACGCCAGGCCAGTGTGTT
TGAAAATTTCTTTTTGGGGGGCAGCAGTTTCTTTTAAACTAAATAATTGTTAC
AAAATAAAA

FIGURE 49

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40571
MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITYAINVSLMWSFRKVQEPQGKAKRHGNTV
PGEWPWQASVRRQGAHICSGSLVADTWVLTAHCFEKAATELNSWSVVLGSLQREGLSPGA
EEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATGWDQDTS
DAPGTLRNLRLRLISRPTCNCIYNQLHQRLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLC
LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAFLAQSPETPEMSDEDS
CVACGSLRTAGPQAGAPSPWPWEARLMHQQLACGGALVSEEAVLTAAHCFIGRQAPEEWSV
GLGTRPEEGLKQLLHGAYTHPEGGYDMALLLAQPVTLGASLRPLCLPYPDHHLPDGERG
WVLGRARPGAGISSLQTVPTLLGPRACSRHLAAPGGDGSPILPGMVCTSAVGELPSCEGLS
GAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVSSLQVYFAEEPEPEAEP
GSCLANISQPTSC

Important features:

Signal peptide:

amino acids 1-15

Homologous region to Serine proteases, trypsin family

amino acids 79-95, 343-359 and 237-247

N-glycosylation sites.

amino acids 37-40 and 564-567

Kringle domains

amino acids 79-96, 343-360 and 235-247

FIGURE 50

CGGGCCGCCCGCCCCCATTGGGCCGCGCTCGCTGGCGGGGACTGAGCCAGGCTGG
GCCGCGTCCCTGAGTCCCAGAGTCGGCGGGCGGGCAGGGGCAGCCTCACACGGGAG
CCCAGCTGTCAGCCGCCTCACAGGAAGATGCTGCGTCGGCGGGCAGCCCTGGCATGGTGT
GCATGTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCCAGG
TCCCTGAAGACCCAGTGGTGGCACTGGTGGCACCGATGCCACCCCTGTGCTGCTCCTCTCC
CCTGAGCCTGGCTTCAGCCTGGCACAGCTAACCTCATCTGGCAGCTGACAGATAACAAACA
GCTGGTGCACAGCTTGCTGAGGGCCAGGACCAGGGCAGCGCTATGCCAACCGCACGGCCC
TCTTCCCGGACCTGCTGGCACAGGGCAACGCATCCCTGAGGCTGCAGCGTGCAGCGTGGCG
GACGAGGGCAGCTTCACCTGCTCGTGAGCATCCGGATTTCGGCAGCGTGCAGCGTCAAGCCT
GCAGGTGGCCGCTCCCTACTCGAAGCCCAGCATGACCCTGGAGGCCAACAAAGGACCTGCGC
CAGGGGACACGGTGACCATCACGTGCTCCAGCTACCAGGGTACCCCTGAGGCTGAGGTGTT
TGGCAGGATGGGCAGGGTGTGCCCTGACTGGCAACGTGACCACGTCGCAGATGGCCAACGA
GCAGGGCTTGTGATGTGCACAGCGTCTGGGGTGGTGCAGGGTGAATGGCACCTACA
GCTGCCTGGTGCACACCCGTGCTGCAGCAGGATGCGCACRGCTCTGTCACCACAGGG
CAGCCTATGACATTCCCCCAGAGGCCCTGTGGGTGACCGTGGGCTGTCTGTCTCAT
TGCACTGCTGGTGGCCCTGGCTTCGTGTGCTGGAGAAAGATCAAACAGAGCTGTGAGGAGG
AGAATGCAGGAGCTGAGGACCAGGATGGGAGGGAGAAGGCTCAAGACAGCCCTGCAGCCT
CTGAAACACTCTGACAGCAAAGAAGATGATGGACAAGAAATGCCTGACCATGAGGACCAGG
GAGCTGCTACCCCTCCCTACAGCTCCTACCCCTGGCTGCAATGGGCTGCACTGTGAGCCC
TGCCCCAACAGATGCATCCTGCTCTGACAGGTGGCTCCTCTCAAAGGATGCGATAACAC
AGACCACGTGCAGCCTTATTCTCCAATGGACATGATTCCAAGTCATCCTGCTGCCTTT
TTCTTATAGACACAATGAACAGACCACCAACCTTAGTTCTCTAAGTCATCCTGCCTGCT
GCCTTATTCACAGTACATACATTTCTTAGGGACACAGTACACTGACCACATCACCACCC
TTCTTCCAGTGCTGCGTGGACCATCTGGCTGCCTTTCTCCAAAGATGCAATATTAGA
CTGACTGACCCCTGCCTTATTCAACAAAGACACGATGCATAGTCACCCGGCCTGTT
TCCAATGGCGTGATACACTAGTGATCATGTTCAGCCCTGCTCCACCTGCATAGAATCTT
TCTTCTCAGACAGGGACAGTGCGGCCTCAACATCTCCTGGAGTCTAGAAGCTGTTCT
CCCTCCTCCCTGCCCAAGTGAAGACAGGGCAGGGCAGGAATGCTTGGGACACCG
AGGGGACTGCCACCCCCCACCAGGTGCTATTCTGGGCTGGGAGTCTAGAAGCTGTTCT
TTGCCTCTGGCCAGCTCCTGGCCTCTGGTAGAGTGAGACTCAGACGTTCTGATGCCTCCG
GATGTCATCTCCCTGCCCAAGGAATGGAAGATGTGAGGACTCTAATTAAATGTCTTGTAAAA
TCGGAGGGATTTGTAAACTGGGGTATATTGGGAAATAATGTCTTGTAAAAAAA
AAAAAAAAAAAAAA

FIGURE 51

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386
><subunit 1 of 1, 316 aa, 1 stop, 1 unknown
><MW: -1, pI: 4.62, NX(S/T): 4
MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTATLCCSFSPEPGFSLAQ
LNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLLAQGNASLRLQRVRVADEGSFTCFV
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGQGVPL
TGNVTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTFPPEA
LWVTVGLSVCLIALLVALAFVCWRKIKQSCEENAGAEDQDGEGEGSKTALQPLKHSDSKED
DGQEIA
```

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 251-270

N-glycosylation site.

amino acids 91-94, 104-107, 189-192 and 215-218

Homologous region to Immunoglobulins and MHC

amino acids 217-234

FIGURE 52

TTCTGTGACCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTCTAAGAAGGGGGAGTC
CTGAACCTTGTCTGAAGCCCTGTCCGTAAGCCTTGAACACTACGTTCTTAAATCTATGAAGTCG
AGGGACCTTCGCTGCTTGTAGGGACTTCTTCCCTGCTTCAGCAACATGAGGCTTTCT
TGTGGAACGCGGTCTTGACTCTGTCACCTCTTGTAGTGGGCTTGTACCCCTGAACCA
GAAGTGAAAATTGAAGTTCTCCAGAAGCCATTCTATCTGCCATCGCAAGACCAAAGGAGGGGA
TTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTCACTCCACTC
ACAAACATAACAATGGTCAGCCCATTGGTTACCCCTGGGCATCCTGGAGGCTCTAAAGGT
TGGGACCAGGGCTGAAAGGAATGTGTAGGAGAGAAGAGAAAGCTCATCATTCCCTGC
TCTGGGCTATGGAAAAGAAGGAAAAGGTTAAAGCATATTCCAGAAAGTACACTGATATTAAATA
TTGATCTCCTGGAGATTGAAATGGACCAAGATCCCCTGAATCATTCCAAGAAATGGATCTT
AATGATGACTGGAAACTCTCTAAAGATGAGGTTAAAGCATATTAAAGAAGGAGTTGAAAAA
ACATGGTGCAGGTGGTGAATGAAAGTCATCATGATGCTTGGTGGAGGATATTGATAAAAG
AAGATGAAGACAAAGATGGTTATATCTGCCAGAGAATTACATATAAACACGATGAGTTA
TAGAGATACATCTACCCCTTTAATATAGCACTCATCTTCAAGAGAGGGCAGTCATCTTAA
AGAACATTTATTTATACAATGTTCTTCTGCTTGTGTTATTTATATATTTTT
CTGACTCCTATTAAAGAACCCCTAGGTTCTAAGTACCCATTCTTCTGATAAGTTATT
GGGAAGAAAAGCTAATTGGTCTTGAATAGAAGACTCTGGACAATTTCACCTTCACAG
ATATGAAGCTTGTAACTTCTCACTTAAATTTAAATGTTGCAACTGGGAATATACC
ACGACATGAGACCAGGGTATAGCACAAATTAGCACCCCTATATTCTGCTTCCCTCTATTTC
TCCAAGTTAGAGGTCAACATTGAAAAGCCTTTGCAATAGCCAAGGCTTGCTATTTCAT
GTTATAATGAAATAGTTATGTGTAAGTGGCTCTGAGTCTCTGCTTGAGGACCAGAGGAAA
TGGTTGTTGGACCTGACTGTTAATGGCTACTGCTTACTAAGGAGATGTGCAATGCTGAAG
TTAGAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCCAGCACTTGGGAG
GCTGAGGCAGGGGAGTACCTGAGGTTGGAGTTGAGACCAGCCTGACCAACACGGAGAAA
CCCTATCTACTAAAATACAAAGTAGCCGGCGTGGTGTAGCGTGCCTGTAATCCCAGCT
ACCCAGGAAGGCTGAGGCCAGAATCACTGAAACCCGAGGCCAGGGTTGGTAAAGCCGAG
ATCACCTNCAGCCTGGACACTCTGTCTCGAAAAAAGAAAAGAACACCGTTAATACCATATNA
ATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGGCTGGCTCTAGTGT
TGGTGGCCTATTATGATAAAATAGGACAAATCATTATGTGTGAGTTCTTGTAAATAAAATG
TATCAATATGTTATAGATGAGGTAGAAAGTTATATTATTCATATTACTTCTTAAGGC
TAGCGGAATATCCTCCTGGTCTTAATGGTAGTCTATAGTATATTACTACAATAACA
TTGTATCATAAGATAAAAGTAGTAAACCAGTCTACATTTCCTCATGCTCATAAAAAC
TGAAGTTAGCTGGTGTGGCTCATGCCTGTAATCCCAGCACTTGGGAGGCCAGGGAGGG
TGGATCACTTGAGATCAGGAGTTCAAGACCAAGCAGCCTGGCCAACATGGTGAACCTTGTCTCA
CTAAAAATACAAAATTAGCCAGGCAGTGGTGGTGACACCTGTAGTCCCAGCTACTCGGGAG
GCTGAGACAGGGAGATTGCTTGAACCCGGGAGGCCAGGGTGCAGTGAGGCCAAGATTGTGCC
ACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAAAAGAACAGA
CCTACAGCAGCTACTATTGAATAAACCTATCCTGGATTT

FIGURE 53

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44194
><subunit 1 of 1, 211 aa, 1 stop
><MW: 24172, pI: 5.99, NX(S/T): 1
MRLFLWNAVLTLFVTSLIGALIPEPEVKIEVLQKPFICHRKTGGDMLVHYEGYLEKD GSL
FHSTHKHNNQPIWFTLGLILEALKGWDQGLKGMCVGEKRKLIIPPALGYGKEGKGKIPPEST
LIFNIDLLEIRNGPRSHESFQEMDLNDDWKLSKDEVKAYLKKEFEKGAVVNESHDALVED
IFDKEDEDKDGFISAREFTYKHDEL
```

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 176-179

Casein kinase II phosphorylation site.

amino acids 143-146, 156-159, 178-181 and 200-203

Endoplasmic reticulum targeting sequence.

amino acids 208-211

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 78-114 and 118-131

EF-hand calcium-binding domain.

amino acids 191-203, 184-203 and 140-159

S-100/ICaBP type calcium binding domain

amino acids 183-203

FIGURE 54

AATAAGCTCCTTAATGTTATATGTTAGTACATCCGTGCATTTTTAGCAT
CCAACCATTCCCTCCTGTAGTTCTCGCCCCCTCAAATCACCTCTCCGTAGCCCACCGA
CTAACATCTCAGTCTCTGAAAATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCT
CACGGGGCTCAGTCTCTTTCTCTTGGTGCACCAGGACGGAGCATGGAGGTACAGTAC
CTGCCACCCCTCAACGTCCTCAATGGCTCTGACGCCCTGCACCTCAACTCCTGC
TACACAGTGAACCACAAACAGTTCTCCCTGAACGGACTTACCAAGGAGTGACAACA
ACTGTC
TGAGGAGATGTTCTCCAGTTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTCAAG
ACCGCGTGGAGTTCTCAGGGAACCCCAGCAAGTACGATGTGCGGTGATGCTGAGAAACGTG
CAGCCGGAGGGATGAGGGGATTACAACGTACATCATGAACCCCCCTGACCGCCACCGTGG
CCATGGCAAGATCCATCTGCAGGTCTCATGGAAGAGCCCCCTGAGCGGACTCCACGGTGG
CCGTGATTGTGGGTGCCTCCGTGGGGCTCCTGGCTGTGGTCATCTGGTGCATGGT
GTCAAGTGTGTGAGGGAGAAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACGGAGGA
GGAGGGCAAGACGGACGGTGAAGGCAACCCGGATGATGGGCCAAGTAGTGGGTGGCCGGCC
CTGCAGCCTCCGTGTCCTCCCTCTCCGCCTGTACAGTGACCCCTGCTCG
CTCTTGGTGTGCTCCGTGACCTAGGACCCCAGGGCCACCTGGGCTCTGAACCCCCG
ACTTCGTATCTCCACCCCTGCACCAAGAGTGACCCACTCTCCATCCGAGAAACCTGCCA
TGCTCTGGGACGTGTGGGCCCTGGGAGAGAGAAAGGGCTCCCACCTGCCAGTCCCTGG
GGGGAGGCAGGAGGCACATGTGAGGGTCCCCAGAGAGAAGGGAGTGGTGGCAGGGTAGA
GGAGGGCCGCTGTCACCTGCCAGTGCTGCCTGGCAGTGGCTTCAGAGAGGACCTGGTGG
GGAGGGAGGGCTTCCTGTGCTGACAGCGCTCCCTCAGGAGGGCCTGGCCTGGCACGGCTG
TGCTCCTCCCTGCTCCCAGCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCTGA
AACTGGAGGGCATGTTAAAGGGATGACTGTGCAATTCCAGGGCACTGACGGAAAGCCAGGG
CTGCAGGCAAAGCTGGACATGTGCCCTGGCCAGGAGGCATGTTGGCCCTCGTTCCATT
GCTAGTGGCCTCCTGGGCTCCTGGCTCTTAATCCCTAGGACTGTGGATGAGGCCAG
ACTGGAAGAGCAGCTCCAGGTAGGGGCATGTTCCCAGCGGGGACCCACCAACAGAGGCC
AGTTCAAAGTCAGCTGAGGGCTGAGGGTGGGCTCCATGGTGAATGCAGGTTGCTGCAG
GCTCTGCCCTCTCCATGGGTAACCACCCCTGCCCTGGCAGGGCAGCCAAGGCTGGAAAT
GAGGAGGCCATGCACAGGGTGGGCAGCTTCTTGGGCTTCAGTGAGAACTCTCCAGTT
GCCCTGGTGGGTTCCACCTGGCTTTGGCTACAGAGAGGGAAAGGCTGAGGCCG
GCATAAGGGAGGGCTGGAACCTGAGCTGCCAATGCCAGCCCTGTCCCATCTGGGCCACG
CTACTCGCTCCTCTCCAAACAACCTCCCTCGTGGGACAAAAGTGACAATTGTAGGCCAGGC
ACAGTGGCTACGCCGTAAATCCAGCACTTGGGAGGCCAAGGCAGGGTGGATTACCTCCAT
CTGTTAGAAATGGGAAAACCCATCTACTAAAAATACAAGAATTAGCTGGCGTG
GTGGCGTGTGCTGTAATCCCAGCTATTGGGAGGCTGAGGAGGAATCGCTTGAGCCCG
GGAAGCAGAGGTTGCAGTGAACGTGAGATAGTGATAGTGCCACTGCAATTAGCCTGGGTGAC
ATAGAGAGACTCCATCTAAAAAA

FIGURE 55

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415
<subunit 1 of 1, 215 aa, 1 stop
<MW: 24326, pI: 6.32, NX(S/T): 4
MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNVLNGSDARLPCTFNSCYTVNHKQ
FSLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMLRNVQPEDEGI
YNCYIMNPPDRHRGHGKIHQLQVLMEPPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRRK
KEQKLSTDDLKTTEEGKTDGEGNPDDGAK
```

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 161-179

Immunoglobulin-like fold:

amino acids 83-127

N-glycosylation sites.

amino acids 42-45, 66-69 and 74-77

FIGURE 56

GTTGTATATGTCCTGAAGTACATCCGTGCATTTTTAGCATCCAACCATCCTCCCTGTA
GTTCTCGCCCCCTCAAATCACCTCTCCCTTAGCCCACCCNACTAACATCTCAGTCTCTGAA
AATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTCAGCCTCACGGGGCTCAGTCTCTTT
TCTCTTGGTGCCACCAGGACGGAGCATGGAGGTCCACAGTACCTGNCCACCCCTAACGTCC
TCAATGGCTCTGACGCCCGCCTGCCCTGCCCTCAACTCCTGCTACACAGTGAACCACAAAC
AGTTCTCCCTGAACTGGACTTACCAAGGAGTGCAACAACGTCTGAGGGAGATGTTCCCTCAG
TTCCCGCATGAAGATCATTAAACCTGAAGCTGGAGCGGTTCAAGACCGCGTGGAGTTCTCAGG
GAACCCCAGCAAGTACGATGTGTCGGTGATGCTGAGAACGTGCAGCCGGAGGATGAGGGGA
TTTACAAC TGCTACATCATGAACCCCCC

FIGURE 57

TCACGGGGCTCATCTTTCTTTGGTGCCACCAGGACGGAGCATGGAGGTNCACATA
CCTGCCACCCCTCAACGTCCCTCAATGGCTTGACGCCCGCTGCCCTGCACCTTCAACTCCNG
CTACACAGTGAACCACAAACAGTTCTCCCTGAACCTGGATTACCAGGAGTGCAACAACTGGC
TCTGAGGAGATGTTCCCTCCAGTTCCCGCATGGAAGATCATTAAACCTGAAAGCTGGAAGCGG
TTTCAGAAACCGCGTGGAAAGTTCTCAGGGAACCCCAGCAAGTACGATGTGTCGGTGATGC
TGAGAAACGTGCAGCCGGAGGATGAGGGGATTACAAC TGCTACATCATGAACCCCCC

1000 900 800 700 600 500 400 300 200 100

FIGURE 58

TGCGGCGACCGTCGTACACCATGGGCCTCCACCTCCGCCCTACCGTGTGGGCTGCTCCGGATGGCCTCCTGT
TCCTCTTGCTGCTGTAATGCTGCTCGGGACCCAGCGCTCCGGCGACGTACCCCCCAGTGGTGTGGTCC
CTGGTGATTGGTAACCAACTGGAAGCCAAGCCAGGCACAGGGTGCACTACCTTGCTCCAAGAAGA
CCGAAAGCTACTTCAAATCTGGCTGAACCTGGAACTGTGTGCCTGTCATATTGACTGTGGATGACAAAT
TCAGGCTGGTTACAACAAAACATCCAGGGCCACCCAGTTCCCTGTATGGGTGGATGTACGTGTCCCTGGTT
GGAAGACCTTCACGTGGATTCGTGGACCCAGCAAAAGCAGCGGTGGTTCCTATTCCACACATGGGGGAG
GCCTGTGGCTGGCTACACACGGGGGTGAGGTTCCGAGGGGGCTCCCTATGACTGGCGCCAGCCAAAT
AAAACGGCCCTACTTCTGGCCCTCCCGAGATGATCAGGGAGATGTACCAGGCTGTATGGGGCCCGGG
TGGTTGGCCACAGTATGGCAACATGTACCGCTCTACTTCTGTCACGGGCGAGCCCTGGAAAGGGACAAGT
ATATCCGGCCCTCGGTCACTGGGTCGCCCTGGGGGGGGCGGTGGCCAAAGACCCGTCGCGGTCTGGCTTCAGGG
ACAAACACGGATCCAGTCATCGGGCCCTGTGAAGATCCGGGAGCAGCGCGGTCAGTGTCTCCACACAGGTGGCC
TGCTGGCCTACAACATACATGGTCACCTGGGAAGGTGTTCGTCGAGACACCCCAATCAACACATGTGG
ACATCCGGCAAGTTCTCCAGGAATCGGGCTTTGAAGATGGGTTCGGCTATGCGGCAGGACACAGGGGTGGTT
AAGCCACGGATGCCACTGGCGGTGCAGCTGCCTCTATGGGTACTGGGTCCCCACACAGACCTCCCTTACT
ATGAAGAGCTCCCTGACGGTGACCCTAAATCTGTTTGGGTACGGGTATGGTACTGTGAACATGAGTGG
TGCAGTGGCCAGGGCTGGCAGGCCGGAGGACCAAGGTTTGTGTCGAGGGAGGTCCCAGGCGAGCAATCG
AGATGTGGCCACCCACCCCTGGCCCTATGTGAACATGTGTGTCTTTGGCCCT**TG**ACTCTGTGCCAAGGA
CTCTGTGGCTCGGGCTGGACCTGTGTTTGGCCCTGGGTGTCAGGCCACCCCGGTTTGCAAAGTTGTGA
CTCACCATCAAGGGCCCGAGGTCTGGACGTGAAGATGTCCATGGGAAGGTGTTTGTATCCTTCTCT
GTGGCAGTGAAGGAAGAAATGAAGGTCTAGACGTCAAGGGGAACGTGGATGGCAGAATGTGTGTATGGGTGG
ACCTGTGTGACTTAGGACGTGGCTCCACAGGGGTGGACGTGGCTGGCCCTGGCTCCGTGGCCAT
TGTCCCCCCTATTCCTGTGGCTTTCACTGTGCCTGGCCCTGGCCCGAGCCCTCTGGATGGGTGT
ACCTGGGTGTGGCTCTGTACCCAGGGGTCCAGGGATCGGTCTGGCCCTGGCCCTGGGTGACCCTCCACACCA
GCCACAGATAGGCCTGCCACTGGGTCAGGGTAGCTAGAGGTGTGGCTCCCTGTGGCTTAGGGTGGCCAG
TGACGTGGCTCCCTGGCGAGCCTAGTAGGTCCCTGCAGGGCGAGGGGTTTGTGTCCTTGTGGTTCCAG
CCCTGGGAATCTCACTCCACCTCCTACCCTCCTTACCCACAGGGAGGCATTAAGCTGTGGATGGGTGGCGAGATGT
CCCCCCAGCCCGAGGGGTGTGTCCAGGGGGCCCTGTATTTCCCTGTGGATGTGTATGGCCCCAGGGACGTGAAGGT
CTCCCTCCACCCCTGGACGTGTGGTTCCTAAGGTGAAGAGGTGGAGGGGTCCATGGCCCTGTGGGAACCTATGGGA
GAAAGGGGAATCCAAAGGAAGCAGGCAAGGTGGCTGCAGCTCCCTGTGAATACCCACCCATCA
CACTGCCCACCCCTGCCCCTAGGGGTCTCACTAGGTACCAAGGTGGGTCAGCACAGGGGTGAGGATGGGGCTCCCTATCCAC
CCCTGGCCAGCCACCCAGCTTAGTGTGGACGTAGCCAGAAATTTGAATGGGGACCCCTGTGGAGAGGGCCAGGGGTCCCC
TGAGGGCCCCCTAGGGGTTTCTGTGTCCCCAGGGGTCCATGGATCTCCCTGTGGCCAGGGGTATGGAG
CAGGGGTGGCTCCTAGGCAGTAGGTCTTAAGGTGGGTGACTGGCCACAGGGCCAGAAAGGGGTACGGCCCTGTAGGT
GGGGGTCCAAAGACGCCCCTCAGGGTGGACGTGAGTGTCTCCACAGGGGTTTCTGTGGCAGTGGATTTCTGT
TTGCATACATGCCTGGCAGTCTCCCTGTGGCCACATGGGGGTCTGTAGGGCCCCACATGGGGGTCTGTAGGCAGGGGTATGTGG
GATTCTGTGAATAAAGTACTGTGGATGTGTAAAAAAAAAAAA

FIGURE 59

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44189
><subunit 1 of 1, 412 aa, 1 stop
><MW: 46658, pI: 6.65, NX(S/T): 4
MGLHLRPYRVGLLPDGLLFLLLLLMLLADPALPAGRHPPVVLVPGDLGNQLEAKLDKPTVVH
YLCSSKKTESYFTIWLNLLELLPVIIDCWIDNIRLVYNKTSRATQFPDGVDVRVPGFGKTFSL
EFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREMIEEMYQ
LYGGPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRVLASGDNNRI
PVIGPLKIREQQRSAVSTSLLPYNTWSPEKVFVQTPTINYTLRDYRKFFQDIGFEDGWLM
RQDTEGLVEATMPPGVQLHCLYGTGVPTPDSFYYESFPDRDPKICFGDGDGTVNLSALQCQ
AWQSRQEHQVLLQELPGSEHIELANATTLAYLKRVLLGP
```

Important features:

Signal peptide:

amino acids 1-28

Potential lipid substrate binding site:

amino acids 147-164

N-glycosylation sites.

amino acids 99-102, 273-276, 289-292 and 398-401

Lipases, serine proteins

amino acids 189-201

Beta-transducin family Trp-Asp repeat

amino acids 353-365

FIGURE 60

CGGACGCGTGGCGGACCGTGGGCGGCAGCGCGACGGGACATGGAGAGCGGG
GCCTACGGCGGGCCAAGGCGGGCGCTCCTCGACCTGCGCGCTCCTGACGCAGCCGCA
GGTGGTGGCGCGCGCGTGTGCTGGTCTCGCCTGATCGTGTCTCCTGCATCTATGGT
AGGGCTACAGCAATGCCACGAGTCTAACGAGATGTACTGCGTGTCAACCGAACGAGGAT
GCCTGCCGCTATGGCAGTGCCATGGGCTGGCCTCCTGCCCTGGCCTTCTTGGT
GGTCGACGCGTATTCCCCCAGATCAGAACGCCACTGACCGCAAGTACCTGGTATTGGT
ACCTGCTCTCAGCTCTGGACCTCCTGTGGTTGGTTCTGCTTCCTCACCAAC
CAGTGGCAGTCACCAACCGAAGGACGTGCTGGGGGCCACTCTGTGAGGGCAGCCAT
CACCTCAGCTCTTCCATCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCT
ACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACCCGGACCCAAACACT
GCCTACGCCCTACCCAGGTGCATCTGTGGACAACACTACCAACAGCCACCCCTCACCCAGAA
CGCGGAGACCACCGAGGGCTACCGCCGCCCCCTGTGTACTTGAGTGGCGTTAGCGTGGAA
GGGGGACAGAGAGGGCCCTCCCTCTGCCCTGGACTTCCATCAGCCTCTGGAACGTCCA
GCCCTCTCTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC
TGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCAGAGGGCTTCAGTCAGCCGCT
CACTCCTCCAGGGCACTTTAGGAAAGGGTTTTAGCTAGTGTTCCTCGCTTTAATGA
CCTCAGCCCCGCCTGCAGTGGCTAGAACGCCAGCAGGTGCCATGTGCTACTGACAAGTGCCT
CAGCTCCCCCGGCCGGTCAGGCCGTGGAGCCGCTATTATCTCGTTCTGCCAAAG
ACTCGTGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTTGTGCTCTCA
CTCAGGTTGCTTCCCTGTGCCACTGCTGTATGATCTGGGGCCACCACCCCTGTGCCGGT
GGCCTCTGGCTGCCTCCCGTGGTGTGAGGGCGGGCTGGTGTCTCATGGCACTTCCCTTG
CTCCCACCCCTGGCAGCAGGAAGGGCTTGCCTGACAACACCCAGCTTATGAAATATT
TGCAGTTGTTACTTAGGAAGCCTGGGAGGGCAGGGTCCCCATGGCTCCAGACTCTGTC
TGTGCCGAGTGTATTATAAAATCGTGGGGAGATGCCCGCCTGGATGCTTTGGAGACG
GAATAAAATGTTTCTCATTCAAAG

FIGURE 61

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48304
<subunit 1 of 1, 224 aa, 1 stop
<MW: 24810, pI: 4.75, NX(S/T): 1
MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFA  
LIVFSCIYGEGYSNAHESKQMYCVFN
RNEDACRYGSAIGVLAFLASAFFLVV  
DAYFPQISNATDRKYLIGD  
LLFSALWTFLWFVGFC
FLTNQWAVTNPKDVLVGADSVRAA  
ITFSFFSIFSWGVLASLAYQ  
RYKAGVDDFIQNYVDPTP
DPNTAYASYPGASVDNYQQPPFTQNAETTEGYQ  
PPP  
VY
```

Important features:

Type II Transmembrane domain:

amino acids 1-45

Other transmembrane domains:

amino acids 74-90, 108-126 and 145-161

N-glycosylation site.

amino acids 97-100

FIGURE 62

GAGCCACCTACCCCTGCTCCGAGGCCAGGCCCTGCAGGGCCTCATCGGCCAGAGGGTATCAGTGAGCAGAAGG**ATG**
CCCGTGGCCGAGGCCCCCAAGGTGGCTGGCGGGCAGGGGACGGAGGTATGGCGAGGAAGGGAGGCCAGAGGG
ATGTTCAAGGCCTGTGAGGACTCCAAGAGAAAAGGCCGGGGCTACCTCCGCTGGTGCCCCCTGTTGTGCTGCTG
GCCCTGCTCGTGTGGCTTCGGCGGGGGTGTACTCTGGTATTCCTAGGGTACAAGGCCAGGTATGGTCAGC
CAGGTGTACTCAGGCAGTCTCGCTGTACTCAATGCCACTCTCCAGGATCTTACCCGCCGGAACTTAGTGCC
TTCGCAGTGAACCCCAAAGCCCAGAAGATGCTAAGGAGCTCATCACCAGCACCCGCTGGGAACTTACTAC
AACTCCAGCTCCGCTATTCCCTTGGGAGGGACCCCTCACCTGCTTCTGGTTCATCTCCAAATCCCCGAG
CACCGCCGGCTGATGCTGAGCCCCGAGGTGGTGCAGGCAGTCTGGTGAGGAGCTGCTCACAGTCACAGC
TCGGCTGCCGTCCCCACAGGCCAGTACGAAGTGGACCCGAGGGCTAGTGTACCTGGAGCCAGGTCTCCGGCTG
GACATAGCTGCATTGAATTCAACGCTGGTTGTACCGCTACAGCTACGTGGGCCAGGGCCAGGTCTCCGGCTG
AAGGGGCTGACCACCTGGCTCCAGCTGCCTGTGGCACCTGCAGGGCCCAAGGACCTCATGCTCAAACCTCCGG
CTGGAGTGGACGCTGGCAGAGTGCCGGACCGACTGGCATGTATGACGTGGCCGGCCCTGGAGAAGAGGCTC
ATCACCTCGGTACGGCTGCAGCCGCCAGGAGCCCGTGGTGGAGGTTCTGGCTCGGGGCCATCATGGCGTC
GTCTGGAAAGAAGGGCTGCACAGCTACTACGACCCCTCTCGTCTCCGTGCAGCCGGTGGTCTTCAGGCCCTGT
GAAGTGAACCTGACGCTGGACACAGGCTCGACTCCAGGGCTCTCAGCACCCGTACTTCCCAGCTACTAC
TCGCCCAAAACCCACTGCTCTGGCACCTCACGGTCCCCCTCTGGACTACGGCTTGGCCCTCTGGTTGATGCC
TATGCACTGAGGAGGCAGAAGTATGATTGCGCTGCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTG
GGCTTGCATCTGCAGCCCTACGCCAGAGGATCCCCGTGGTGGCCACGGCCGGATCACCATCAACTCACC
TCCCAGATCTCCCTCACCGGGCCGGTGTGGGGTGCACTATGGCTGTACAACCAGTCGGACCCCTGCCCTGGA
GAGTTCTCTGTTCTGTGAATGGACTCTGTGATGGGTCAAGGACTGCCAACGGCTGGAT
GAGAGAAACTGCGTTGCAGAGCCACATCCAGTGCACAGGAGGACAGCACATGCATCTCACTGCCAACGGTCTGT
GATGGGCAGCCTGATTGCTCAACGGCAGCGATGAAGAGCAGTGCAGGAAGGGTGCCTGTGGGACATTCA
TTCCAGTGTGAGGACCGGAGCTGCGTGAAGAAGCCAACCCCGAGTGTGATGGGCGGCCACTGCAGGGACGGC
TCGGATGAGGAGCACTGTGACTGTGGCTCCAGGGCCCTCCAGCCGATTGTTGGTGGAGCTGTCTCCGAG
GGTAGTGGCATGGCAGGCCAGCCTCAGGTTGGGTCGACACATCTGTGGGGGGCCCTCATCGCTGACCGC
TGGGTGATAACAGCTGCCACTGCTTCCAGGAGGACAGCATGGCTCCACGGTGTGGACCGTGTCTGGG
AAGGTGTGGCAGAACTCGCCTGGCTGGAGAGGTGTCTCAAGGTGAGCCGCTGCTCCTGCACCCGTAC
GAAGAGGACAGCCATGACTACGACGTGGCCTGCTGCAGCTCGACCACCCGGTGGCGCTGGCCGGTGC
CCCGTCTGCCTGCCCGCGCTCCACTCTCGAGCCGGCTGACTGCTGGATTACGGCTGGGGCGCCTTG
CGCGAGGGCGGCCCATCAGAACGCTCTGCAGAAAGTGGATGTGCAGTTGATCCACAGGACCTGTGCAGCGAG
GCCTATCGCTACCAGGTGACGCCACGCATGCTGTGCGGGCTACCGCAAGGGCAAGAAGGATGCCCTGT
GACTCAGGTGGTCCGTGGTGTGCAAGGGACTCAGTGGGGCTGGTCTGGGGCTGGTCAAGGCTGGGGCTG
GGCTGTGGCCGGCTTAACTACTCGGGCTCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGT
AC**TG**AGGAAGTGCCTCTGCAAAGCAGGGCCACCTCTGGACTCAGAGAGGCCAGGGCAACTGCCAACGAGG
GGGACAAGTATTCTGGCGGGGGTGGGGAGAGAGCAGGCCCTGTGGTGGCAGGAGGTGGCATCTGTCTCGTCC
CTGATGTCGCTCCAGTGATGGCAGGAGGATGGAGAAGTGCAGCAGCTGGGGTCAAGACGCTCCCTGAGGACC
CAGGCCACACCCAGCCCTCTGCCCTCCAAATTCTCTCCGCTCCCTTCCACTGCTGCCATAATGCAAG
GCAGTGGCTCAGCAGCAAGAATGCTGGTCTACATCCCAGGGAGTGTCTGAGGTGCGCCCCACTCTGTACAGAGG
CTGTTGGCAGCCTGCTCCAGAGAGCAGATTCCAGTCTGGAGGCCCTGGTCAACTTGGATCTGGGAAT
GGAAGGTGCTCCATCGGAGGGGACCCCTCAGAGCCCTGGAGACTGCCAGGTGGGCTGCTGCACGTAA
AAGGTGGGAAGTCCTGACTCCAGGGTCTTGGCCCCACCCCTGCCACCTGGCCCTCACAGCCAGACCC
CACTGGGAGGTGAGCTCAGTGCCTTGGATAAAGCTGCCCTGATCAAAAAAAAAAAAAAA

FIGURE 63

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152
><subunit 1 of 1, 802 aa, 1 stop
><MW: 88846, pI: 6.41, NX(S/T): 7
MPVAEAPQVAGGQGDGGDGEAEPEGMFKACEDSKRKARGYLRLVPLFVLLALLVLASAGVL
LWYFLGYKAEVMVSQVYSGSLRVLRHFSQDLTRRESSAFRSETAKAQKMLKELITTRLGT
YYNSSSVYSFGEGPLTCFFWFILQIPEHRRMLSPVVQALLVEELLSTVNSSAAVPYRAEY
EVDPEGLVILEASVKDIAALNSTLGCYRYSYVGQGQVRLKGPDHASSCLWHLQGPKDML
KLRLEWTLAECRDRLLAMYDVAGPLEKRLITSVYGCSRQEPPVVEVLASGAIMAVVWKKGLHSY
YDPFVLSVQPVVFQACEVNLTLDNRLDSQGVLSPTYFPSYYSPQTHCSWHLTVPSLDYGLAL
WFDAYALRRQKYDLPCTQGQWTIQNRRLCGLRILQPYAERIPVVAAGITINFTSQISLTGP
GVRVHYGLYNQSDPCPGFCLCSVNGLCVPACDGVKDCPNGLDERNCVRATFQCKEDSTCIS
LPKVCDGQPDCLNGSDEEQCQEGVPCGTFTFQCEDRSCVKKPNPQCDGRPDCRDGSDEEHCD
CGLQGPSSRIVGGAVSSEGEWPWQASLQVGRRHICGGALIADRWTAAHCFQEDSMASTVL
WTVFLGKVWQNSRWPGEVSKVSRLLLHPYHEEDSHDYDVALQLDHPVVRSAAVRPVCLPA
RSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCSEAYRYQVTPRMLCAGYRKG
KKDÄCQGDGGPLVCKALSGRWFLAGLVSWGLGCRPNYFGVYTRITGVISWIQQVVT

Important features:

Type II transmembrane domain:

amino acids 46-67

Serine proteases, trypsin family, histidine active site.

amino acids 604-609

N-glycosylation sites.

amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447
and 509-512

Kringle domains.

amino acids 746-758 and 592-609

Homologous region to Kallikrein Light Chain:

amino acids 568-779

Homologous region to Low-density lipoprotein receptor:

amino acids 451-567

FIGURE 64

GCACCCAGGCCAGTGGACGATCCAGAACAGGAGGCTGTGGCTTGCATCCTGCAGCCC
TACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTCACCTCCAGAT
CTCCCTCACCGGGCCCGGTGTGCAGGGTGCAGTATGGCTGTACAACCAGTCGGACCCCTGCC
CTGGAGAGTTCTCTGTTCTGTGAATGGACTCTGTGTCCCTGCCTGTATGGGTCAAGGAC
TGCCCCAACGGCTGGATGAGAGAAACTGCAGTGCAGAGCCACATTCCAGTGCAGAACAGGAA
CAGCACATGCATCTCACTGCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCG
ATGAAGAGCAGTGCAGGAAGGGTGCATGTGGACATTCACCTCCAGTGTGAGGACCGG
AGCTGCGTGAAGAACGCCAACCCGCAGTGTGATGGGCAGCCACTGCAGGGACGGCTCGGA
TGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCTCCAGCCGCATTGTTGGTGGAGCTGTG
CCTCCGAGGGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTGGTCGACACATCTGTGG
GGGCCCTCATCGCTGACCGCTGGTGATAACAGCTGCCACTGCTCCAGGAGGACAGCAT
GGCCTCACGGTGTGGACCGTGTGGCAAGGTGTGGCAGAACACTCGCGCTGGCCTG
GAGAGGTGTCTTCAAGGTGAGCCGCTGCTGCAGCTCGACCACCCGGTGGCGCTCGGCC
GACTACGACGTGGCGCTGCTGCAGCTCGACCACCCGGTGGCGCTCGGCC
CGTCTGCCTGCCCGCGCTCCCACCTCTCGAGCCGGCCTGCAGTGGATTACGGCT
GGGCGCCTTGGCGAGGGCGGCCATCAGCAACGCTCTGCAGAAAGGGATGTGCAGTTG
ATCCCACAGGACCTGTGCAGCGAGGCCTATCGCTACCAGGTGACGCCACGCATGCTGTG
CGGCTACCGCAAGGGCAAGAACGGATGCCTGTCAGGGTACTCAGGTGGTCCGCTGGTGTG
AGGCACTCAGTGGCGCTGGTCTGGCGGGCTGGTCAGCTGGGCTGGCTGTGGCCGG
CCTAACTACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGG
GACCTGAGGAAGTGCCTCTGCAAAGCAGGGCCACCTCTGGACTCAGAGAGCCAGGGC
AACTGCCAAGCAGGGGACAAGTAT

FIGURE 65

GGACGAGGGCAGATCTCGTTCTGGGGCAAGCCGTTGACACTCGCTCCCTGCCACCGCCCGGG
CTCCGTGCCGCCAAGTTTCATTTCCACCTTCTGCCTCCAGTCCCCCAGCCCCCTGGCCG
AGAGAAGGGTCTTACCGGCCGGATTGCTGGAAACACCAAGAGGTGGTTTGTTTAAA
ACTTCTGTTCTGGGAGGGGTGTGGCGGGCAGGATGAGCAACTCCGTTCTGCTCTG
TTTCTGGAGCCTCTGCTATTGCTTGCTGCGGGAGCCCCGTACCTTGTCCAGAGGGAC
GGCTGGAAGATAAGCTCCACAAACCAAAGCTACACAGACTGAGGTCAAACCATCTGTGAGG
TTAACCTCCGCACCTCCAAGGACCCAGAGCATGAAGGATGCTACCTCTCCGTCGGCACAG
CCAGCCCTTAGAAGACTGCAGTTCAACATGACAGCTAAACCTTTCATCATTACGGAT
GGACGATGAGCGGTATCTTGAAACTGGCTGCACAAACTCGTGTCAAGCCCTGCACACAAGA
GAGAAAGACGCCAATGTAGTTGTGGTTGACTGGCTCCCCCTGGCCCACCAGCTTACACGGA
TGCGGTCAATAATACCAGGGTGGTGGACACAGCATTGCCAGGATGCTGACTGGCTGCAGG
AGAAGGACGATTCTCTCGGAATGTCCACTTGATCGGCTACAGCCTCGGAGCGCACGTG
GCCGGGTATGCAGGCAACTCGTGAAGGAACGGTGGCCGAATCACAGGTTGGATCCTGC
CGGGCCCATGTTGAAGGGGCCGACATCCACAAGAGGTCTCTCCGGACGATGCAGATTTG
TGGATGTCCTCCACACCTACACGCGTTCTCGGCTTGAGCATTGGTATTAGATGCCTGTG
GGCCACATTGACATCTACCCCAATGGGGTGACTTCCAGCCAGGCTGTGGACTCAACGATGT
CTTGGGATCAATTGCATATGGAACAATCACAGAGGTGGTAAATGTGAGCATGAGCGAGCCG
TCCACCTCTTGTGACTCTGGTGAATCAGGACAAGCCGAGTTGCCTCCAGTGCAC
GACTCCAATCGCTCAAAAAGGGATCTGTCTGAGCTGCCGCAAGAACCGTTGAATAGCAT
TGGCTACAATGCCAAGAAAATGAGGAACAAGAGGAACAGCAAAATGTACCTAAAACCGGG
CAGGCATGCCTTCAGAGGTAAACCTCAGTCCCTGGAGTGTCCCTGAGGAAGGCCCTAATA
CCTCCTCTTAATACCATGCTGCAGAGCAGGGCACATCCTAGCCAGGAGAACGTGGCCAGCA
CAATCCAATCAAATCGTTGCAAATCAGATTACACTGTGCATGTCTAGGAAAGGAAATCTT
ACAAAATAAACAGTGTGGACCCCTAATAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAA

FIGURE 66

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49646
><subunit 1 of 1, 354 aa, 1 stop
><MW: 39362, pI: 8.35, NX(S/T): 2
MSNSVPLLCFWSLCYCFAAGSPVPFGPEGRLEDKLHKPKATQTEVKPSVRFLRTSKDPEHE
GCYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSAHTREKDANVVVDWL
PLAHQLYTDAVNNTRVVGHSIARMLDWLQEKKDDFLGNVHLIGYSLGAHVAGYAGNFVKGT
GRITGLDPAGPMFEGADIHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIVPNGDF
QPGCGLNDVLGSIAYGTITEVVKCEHERAVHLFVDSLNVQDKPSFAFQCTDSNRFKKGICL
CRKNRCNSIGYNAKKMRNKRNSKMYLKTRAGMPFRGNLQSLECP
```

Important features:

Signal peptide:

amino acids 1-16

Lipases, serine active site.

amino acids 163-172

N-glycosylation sites.

amino acids 80-83 and 136-139

FIGURE 67

CGGACGCGTGGCGGACCGTGGCCTGGCAAGGGCGGGCGCCGAGCCACCTCTTCCCCTCCCCGC
TTCCTGCGCCTCGCTGGCTGGACCGCTGGAGGAGTGGAGCAGCACCCGGCCCTGGGGCTGACAGT
CGGCAAAGTTGGCCGAAGAGGAAGTGGTCTCAAACCCGGCAGGTGGCACCAGGCCAGACCGAGGGCGCTCG
CTGCCTGCGGGCGGCTGTAGGCAGGGCGCCCGAGTGCAGGACCCGGGCTTCAGGAGCCGGCCCGGGAG
AGAAGAGTGCAGGGCGGACGGAGAAAACAACCTCAAAGTGGCAAGGCACCGCCCTACTCCCAGGGCTGCG
CCGCCTCCCCGCCCGAGCCCTGGCATCCAGAGTACGGGTCGAGCCGGCATGGAGCCCCCTGGGAGGG
CACCAAGGGAGCCTGGCGCCGGGCTCGCCGCACCCATGGTAGACCACAGAAGCTCCGGACCCTCCG
GCACCTCTGGACAGCCCAGGATGCTGTTGCCACCCCTCCCTCCTGGAGGCGCTCTGGCCATCCAG
ACCGGATTATTTTCAAATCATGCTTGTGAGGACCCCCAGCAGTGCCTTAAAGTGCAGGGCACCTACAGA
GGCCCTGGTCCGGACAGCCACCTCCCTGCCAACACTGCACCTGGCTCATCTGGCAGCAAGGAACAGACTG
TCACCATCAGGTTCCAGAAGCTACACCTGGCTGTGGCTCAGAGCCTTAACCCACTGCTCCCTCCAGCAC
TGATCTCCCTGTGTGAGGACCCCTCCAGGCCCTGCAGCTGCCGGGCAACGTACCATCACTACAGCTATG
CTGGGGCAGAGCACCCATGGCCAGGGCTTCTGCTCTACAGCCAAGATTGGCTGATGCGCTGAGGAAG
AGTTTCAGTGCCTGAACCACCCGCTGTGTATCTGCTGTCAGCCGCTGTGATGGGTTGATGCCGTGGCAGATGGCT
CTGATGAAGCAGGTTGCAGCTCAGACCCCTTCCCTGGCCTGACCCAGGACCCGTCCTCCCTGCCTGCAATG
TCACCTGGAGGACTTCTATGGGTCTTCCCTCCTGGATATAACACACTAGCTCAGTCTCCACCCACCCAGT
CCTGCCATTGGCTGGACCCCCATGATGGCCGGGCTGGCGCTTCACAGCCCTGGACTGGCTTGGCTTGG
GAGATGCAGTGCATGTGTATGACGGGCTGGCCCCCTGAGAGCCTCCGACTACTGCGTAGTCTCACCACTTCA
GCAATGGCAAGGCTGTCAGTGAGACACTGTCTGGCAGGCTGTTGTGCTTACACACAGTTGCTTGAGA
ATGGCTGTTCAATGCCACCTACCATGTGCGGGCTATTGCTGCCCTGGACAGACCCGTGGCTTAGGCT
CTGGCCTGGAGCTGGCAAGGCCTAGGTGAGCCTGCTACAGTGAGGACAGCCTGTCAGGCTCATGGGACT
GTGCTGACGGCACAGATGAGGAGACTGCCAGGCTGCCACCTGGACACTTCCCTGTGGGCTGCTGGCACCT
CTGGTGCACAGCCTGCTACCTGCCCTGCTGACCGCTGCAACTACCAGACTTCTGTGCTGAGCAGATGAGA
GACGCTGCGGATTGCCAGGCTGGCAATTCCGATGCCGGACGAGAAGTGCCTGATGAGACGTGGGTGCG
ATGGCAGCCAGACTGTGCGGACGGCAGTGATGAGTGGACTGCTCTATGTTCTGCCCTGGACAGGTATTACAG
CTGCACTATTGGCAGCCTAGTGTGCGGCTGCTCTGGTATGCCCTGGCTGACACTGCAAGCTATGCCA
TTGCACCCAGGAGTACAGCATTTGCCCTCCGGATGGAGGCTGAGATTGTGAGCAGCAGGACCC
CTTCCCTACGGGAGCTCATTGCCAGGGTGCCTCCACCTGTAGAAGACTTCCCTACAGAGAATCTAATGATA
ACTCAGTGCCTGGCAACCTGCGTTCTGCTACAGATCTTACGCCAGGATATGACTCCAGGAGGTGGCCAGGTG
CCCGCGTCTGCTAGCGGGGCGCTTGATGCGACGCCCTGGTACGCCCTCCGCCGCTGGGCTTGTCCCTCGAA
CCAACACCCCGCTGGGCTCTGAGGCCAGATCCAGGTACACCTCTGCTGCTCCCTGAGGCCCTAGATG
GTGGCACAGGTCCAGCCGTGAGGGCGGGCAGTGGTGGCAAGATGGGAGCAGGACCCACTGCCATCA
AGGCTCCCTCCCTGCTAGCAGCTCCAGCCCCACTACTGTCCTGAAAGCCCCAGGGCACTGCCCTCAC
TGCCCTAGAGCCATCACTATTGTCTGGAGTGGTGCAGGCCCTGCGAGGCCCTGTTGCCCTGCGCTGGGCCCC
CAGGACCAACCCGGAGCCCCCTGGACCCACACAGCAGTCTGCCCTGGAGGAGATGTGCTACTGG
TGCCACTGGCTGAGCCGGGGGTGTGGGTAGCTGAGGAGCAGGAGATGAGCCACTGCTTACCTGAGGGGACCTGGGG
CTCTACTGAGGCCTCTCCCTGGGGCTACTCATAGTGGCACAAACCTTTAGAGGTGGTCAAGCTCCCTCC
ACCACTCCCTCCCTGCTGGATTCAGGGACTGGTGGGCCCTCCGTTGACCCCTATGTAGCTGCTATAAAGT
TAAGTGTCCCTCAGGCAGGGAGAGGGCTCACAGAGTCTCTGTACGTGGCCATGGCAGACACCCAGTCCCT
TCACCACCACTGCTCCCCACGCCACCACATTGGGTGGCTTTAAAGTAAAGTCTTAGAGGATCAT
GGTCTGGACACTCCATCCTGCCAAACCTTACCAAAAGTGGCCTTAAGCACCGGAATGCCAATTAACAGAGA
CCCTCCAGCCCCAAGGGAGGATTGGCAGAACCTGAGGTTTGCCATCCACAATCCCTACAGGGCCTGG
CTCACAAAAAGAGTGCACAAATGCTTCTATTCCATAGCTACGGCATTGCTCAGTAAGTTGAGGTAAAAATAAA
GGAATCATACATCTC

FIGURE 68

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631
<subunit 1 of 1, 713 aa, 1 stop
<MW: 76193, pI: 5.42, NX(S/T): 4
MLLATLLLLLGGALAHPDRIIFPNHACEDPPAVLLEVQGTLQRPLVRDSRTSPANCTWLIL
GSKEQTVTIRFQKLHLACGSERLTLRSPLQPLISLCEAPPSPLQLPGGNVTITYSYAGARAP
MGQGFLLSYSQDWLMCLQEEFQCLNHRCVSQVRCGDGVDACGDGSDEAGCSDPFPGGLTPRP
VPSLPCNVTLDFYGVFSSPGYTHLASVSHPQSCHWLLDPHDGRRLAVRTALDLGFGDAVH
VYDGPGPPESSRLLRSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGNATYHVRGYCLP
WDRPCGLSGLGAGEGLGERCYSEAQRCDGWSDCADGTDEEDCPGCPPGHFPCGAAGTSGAT
ACYLPADRCNYQTFCADGADERRCRHCQPGNFRCRDEKCVYETWVCDGQPDCADGSDEWDCS
YVLPRKVITAAVIGSLVCGLLVIAGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSY
GQLIAQGAIPPVVEDFPTENPNDNSVLGNLRSLLQILRQDMTPGGPGARRRQRGRLMRRLVR
RLRRWGLLPRNTPARASEARSQVTPSAAPLEALDGGTPAREGGAVGGQDGEQAPPLPIKA
PLPSASTSPAPTVPEAPGPLPSLPLEPSLLSGVVQALRGRLLPSLGPPGptrsppgPHTAV
LALEDEDDVLLVPLAEPGVWVAEAEDEPLLT
```

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 442-462

LDL-receptor class A (LDLRA) domain proteins

amino acids 411-431, 152-171, 331-350 and 374-393

FIGURE 69

CGAGCTGGCGAGAAGTAGGGAGGGCGGTGCTCCGCCGCGTGGCGGTTGCTATCGCTTCG
CAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCA
GACGCGATGGATAACGTGCAGCCAAAATAAAACATGCCCTCTGCTTCAGTGTGAAAGG
CCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCTTTTATCATCGCAC
AAGCCCCTGAACCATATATTGTTATCACTGGATTGAAGTCACCGTTATCTTATTTTCATA
CTTTTATATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTGGCCTTGCTTGATAT
TATCAACTCACTGGTAACAAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAG
AAACCACAAACATTGACAGTTGGAGGGGTGTTGCACTTGTGACAGCAGTATGCTGTCTT
GCCGACGGGGCCCTTATTACCGGAAGCTCTGTTCAATCCCAGCGGTCTTACCAAGAAAAAA
GCCTGTGCATGAAAAAAAAGAAGTTTGTAATTTATATTACTTTAGTTGATAACTAAGT
ATTAAACATATTCTGTATTCTTCCAAAAAAAAAAAAAAA

0
9
8
7
6
5
4
3
2
1
0

FIGURE 70

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49645
><subunit 1 of 1, 152 aa, 1 stop
><MW: 17170, pI: 9.62, NX(S/T): 1
MDNVQPKIKHRPFCFSVKGHVKMLRLALTTSMTFFIIAQAPEPYIVITGFEVTVILFFILL
YVLRLDRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTLTVGGGVFALVTAVCCLAD
GALIYRKLLFNPSGPYQKKPVHEKKEVL
```

Important features:

Potential type II transmembrane domain:

amino acids 26-42

Other potential transmembrane domain:

amino acids 44-65, 81-101 and 109-129

Leucine zipper pattern

amino acids 78-99 and 85-106

N-myristoylation site.

amino acids 110-115

Ribonucleotide reductase large subunit protein

amino acids 116-127

FIGURE 71

GGCGAGAAGTAGGGAGGGCGTGTCCGCCGCGGTGGCGTTGCTATCGTTGCAGAAC
TACTCAGGCAGCCAGNTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCAGACGCGA
TGGATAACGTGCAGCCGAAAATAAACATCGCCCCCTCTGCTTCAGTGTGAAAGGCCACGTG
AAGATGCTGCGGCTGGCACTAACTGNGACATCTATGACCTTTTATNATCGCACAAGCCCC
TGAACCATAATTGTTATCACTGGATTGAAAGTCACCGTTATCTTATTTTCATACTTTAT
ATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTGGCCTTGCTTGATATTATCAAC
TCACTGGTAACAACAGTATTGCTCATCGTATCTGTGTGGCACTGATAACCAGAAACCAC
AACATTGACAGTTGGTGGAGGGGTGTTGCACTTGTGACAGCAGTATGCTGTNTTGCACGAC

1000 900 800 700 600 500 400 300 200 100

FIGURE 72

CAGCCCCGCGCGCCGGCCGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGG
CTGGCGCGCCCCCGGGCCCCGGCGTGGCATGGCGCACTGGCCGGCGCTGCTGCTGC
CTCTGCTGGCCAGTGGCTCCTGCGCGCCGGAGCTGGCCCCGCGCCCTCACGCTG
CCCCTCCGGGTGGCCGGCCACGAACCGCGTAGTTGCGCCCACCCGGGACCCGGACCCC
TGCCGAGCGCCACGCCACGGCTTGGCGCTGCCCTGGAGCCTGCCCTGGCGTCCCCGG
GCGCCGCAACTTCTTGGCATGGTAGACAACCTGCAGGGGACTCTGGCCGGCTACTAC
CTGGAGATGCTGATGGGACCCCCCGCAGAAGCTACAGATTCTCGTGACACTGGAAGCAG
TAACTTGCCGTGGCAGGAACCCGCACTCCTACATAGACACGTACTTGACACAGAGAGT
CTAGCACATACCGCTCCAAGGGTTGACGTACAGTGAAGTACACACAAGGAAGCTGGACG
GGCTTCGTTGGGAAGACCTCGTACCATCCCCAAGGCTCAATACTTCTTGTCAA
CATTGCCACTATTTTGAAATCAGAGAATTCTTTGCCTGGATTAAATGGAATGGAATAC
TTGGCCTAGCTTATGCCACACTGCCAACCATCAAGTTCTCTGGAGACCTTCTCGACTCC
CTGGTACACAAGCAAACATCCCCAACGTTCTCCATGCAGATGTGTGGAGCCGGCTTGCC
CGTTGCTGGATCTGGACCAACGGAGGTAGTCTTGCTTGGGTGGAATTGAACCAAGTTGT
ATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTG
AAATTGGAATTGGAGGCCAACGCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC
CATCGTGGACAGTGGCACCACGCTGCTGCCCTGCCAGAAGGTGTTGATGCGGTGGTGG
AAGCTGTGGCCCGCGCATCTGATTCCAGAATTCTCTGATGGTTCTGGACTGGTCCCAG
CTGGCGTGCTGGACGAATCGGAAACACCTGGTCTTACTTCCCTAAATCTCCATCTACCT
GAGAGACGAGAACTCCAGCAGGTCAATTCCGTATCACAATCCTGCCTCAGCTTACATTCA
CCATGATGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCATCCACAAAT
GCGCTGGTATCGGTGCCACGGTGATGGAGGGCTTCTACGTATCTCGACAGAGCCCAGAA
GAGGGTGGGCTTCGCAGCGAGCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATT
CCGGGCCTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTGAGCGAG
CCCATTGTGGATTGTGTCCTATCGCCTCATGAGCGTCTGTGGAGCCATCCTCTGTCTT
AATCGCCTGCTGCTGCCGTTCCGGTGTCAAGCGTCGCCCGTGAACCTGAGGTGTC
ATGATGAGTCCTCTGGTCAGACATCGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAA
CCATGAACCTAGCTATTAAGAAAATCACATTCCAGGGCAGCAGCCGGATCGATGGTGGCG
CTTTCTCCTGTGCCACCCGTCTCAATCTGCTCCAGATGCCTCTAGATTCA
TGTCTTTGATTCTGATTTCAAGCTTCAAATCCTCCCTACTTCCAAGAAAAATAATTAA
AAAAAAACTTCATTCTAA

FIGURE 73

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493
><subunit 1 of 1, 518 aa, 1 stop
><MW: 56180, pI: 5.08, NX(S/T): 2
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ALEPALASPAGAANFLAMVDNLQGDGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHS
YIDTYFDTERSSTYRSKGFDTVVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESENF
FLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGS
LVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLCREYNADKAIVDSGTTLLR
LPQKVFDAVVEAVARASLIPEFSDGFWTGSQLACWTNSETPWSYFPKISIYLRDENSSRSFR
ITILPQLYIQPMMGAGLNYECYRGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCA
EIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCGAILLVLIVLLLLPFRC
QRRPRDPEVVNDESSLVRHRWK
```

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 466-494

N-glycosylation sites.

amino acids 170-173 and 366-369

Leucine zipper pattern.

amino acids 10-31 and 197-118

Eukaryotic and viral aspartyl proteases

amino acids 109-118, 252-261 and 298-310

FIGURE 74

CGCCTCCGCCTCGGAGGCTGACGCGCCGGCGCCGTTCCAGGCCTGTGCAGGGCGGATCG
GCAGCCGCCTGGCGGCGATCCAGGGCGGTGCGGGGCTGGCGGGAGCCGGAGGCGCGGCC
GGCATGGAGGGCGCTGCTGCTGGCGCGGGTTGCTGCTGGCGCTTACGTGCTTGTCTACTA
CAACCTGGTGAAGGCCCGCCGTGCGCGGCATGGCAACCTGCAGGGCCGACGGCGTGG
TCACGGCGCCAACAGCGCATCGGAAAGATGACGGCGCTGGAGCTGGCGCCGGAGCG
CGCGTGGTGCCTGCCGAGCCAGGAGCGCGGGAGGCAGCTGCCTGACCTCCGCCA
GGAGAGTGGGAACAATGAGGTACATCTTACATGGCCTTGGACTTGGCCAGTCTGGCCTCGGTGC
GGGCCTTGCCACTGCCTTCTGAGCTCTGAGCCACGGTGGACATCCTACATCCACAATGCC
GGTATCAGTTCTGTGGCCGGACCCGTGAGGCAGTTAACCTGCTGCTCGGGTAACCATAT
CGGTCCCTTCTGCTGACACATCTGCTGCTGCCTGAAGGCATGTGCCCTAGCCGCG
TGGTGGTGGTAGCCTCAGCTGCCACTGTCGGGACGTCTGACTCAAACGCCCTGGACCGC
CCAGTGGTGGCTGGCGCAGGAGCTGCGGCATATGCTGACACTAAGCTGGCTAATGTACT
GTTTGCCTGGGAGCTGCCAACAGCTTGGAGGCCACTGGCGTCACCTGCTATGCAGCCCACC
CAGGGCCTGTGAACCTGGAGCTGTTCTGCGCCATGTTCTGGATGGCTGCGCCACTTTG
CGCCCATTGGCTGGCTGGTGCCTGGGACCAAGAGGGGTGCCAGACACCCCTGTATTG
TGCTCTACAAGAGGGCATCGAGCCCTCAGTGGAGATATTTGCCAACTGCCATGTGGAAG
AGGTGCCTCCAGCTGCCGAGACGACCGGGCAGCCATGGCTATGGAGGCCAGCAAGAGG
CTGGCAGGGCTTGGCCTGGGAGGATGCTGAACCGATGAAGACCCCCAGTCTGAGGACTC
AGAGGCCCATCTCTCTAACCTCAGGCCAGGATGCTGCCATGGCACTTCATGGCCTT
CCAGCCCTCAGAGCTCACCAGATTGCTAAGATGACGACCGAATTCAAGCTAAAGTTGAG
CCTGAGATCCAGCTCTCTAACCCTCAGGCCAGGATGCTGCCATGGCACTTCATGGCCTT
GAAAACCTCGGATGTGTGAGGCCATGCCCTGGACACTGACGGTTGTGATCTTGACCTC
CGTGGTTACTTCTGGGCCCCAAGCTGTGCCCTGGACATCTCTTCTGGTTGAAGGAAT
AATGGGTGATTATTCTTCTGAGAGTGACAGTAACCCAGATGGAGAGATAGGGTATGCT
AGACACTGTGCTCTCGAAATTGGATGTAGTATTTCAAGGCCACCCCTATTGATTCTG
ATCAGCTCTGGAGCAGAGGCAGGGAGTTGCAATGTGATGCACGCCAACATTGAGAATTAG
TGAAC TGATCCCTTGCAACCGTCTAGCTAGGTAGTTAAATTACCCCTGTTAATGAAGCG
GAATTAGGCTCCGAGCTAAGGGACTGCCCTAGGGTCTCACAGTGAGTAGGAGGAGGGCCTG
GGATCTGAACCCAAAGGGTCTGAGGCCAGGGCGACTGCCGTAAGATGGGTGCTGAGAAGTG
GTCAGGGCAGGGCAGCTGGTATCGAGGTGCCCATGGAGTAAGGGACGCCCTCCGGCG
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FIGURE 75

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss..DNA48227
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VVLACRSQERGEAAAFDLRQESGNNEVIFMALDLASLASVRAFATAFLSSEPRLDILIHNAG
ISSCGRTREAFNLLLRVNHIGPFLTHLLLPCLKACAPSRRVVVASAAHCRGRFLDKRLDRP
VVGWRQELRAYADTKLANVLFARRELANQLEATGVTCYAAHPGPVNSELFLRHVPGLRPLL
PLAWLVLRAPRGGAQTPLYCALQEGIEPLSGRYFANCHVEEVPPAARDDRAHRLWEASKRL
AGLGPGEDAEPDEDPQSEDSEAPSSLSTPHPEEPTVSQPYPSHQSSPDLSKMTHRIQAKVEP
EIQLS
```

Important features:

Signal peptide:

amino acids 1-16

Glycosaminoglycan attachment site.

amino acids 46-49

Short-chain alcohol dehydrogenase family

amino acids 37-49 and 114-124

FIGURE 76

FIGURE 77

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404
<subunit 1 of 1, 985 aa, 1 stop
<MW: 105336, pI: 6.55, NX(S/T): 7
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DTLQLLQPPARGHAHDGQALSTDGVYCEASNRLGTAWSRGARLSVAVLREDFQIQPRDM
VAVVGEQFTLECGPPWGHPEPTVSWWDGKPLALQPGRTVSGGSLLMARAEKSDEGTYMCV
ATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDAEGPKPRPAVWLSWKV
SGPAAPAQSYTALFRQTAPGGQGAPWAEELLAGWQSAELGGLHWGQDYEFKVRPSSGRARG
PDSNVLLLRLPEKVPSAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWSLGNDSLPP
ANWTVVGEQTQLEIATHMPGSYCVQVAVTGAGAGEPSRPVCLLLEQAMERATQEPSEHGPW
TLEQLRATLKRPEVIATCGVALWLLLLTAVCIHRRRRARVHLGPGLYRYTSEDAILKHRMD
HSDSQWLADTWRSTSGSRDLSSSSSLSSRLGADARDPLDCRRSLLWDSRSPGVPLLPDTST
FYGSLLAELPSSTPARPSPQVPAVRRLPPQLAQLSSPCSSSDSLCSRRGLSSPRLSLAPAEA
WKAKKKQELQHANSPLLRGSHSLELRACELGNRGSKNLSQSPGAVPQALVAWRALGPKLLS
SSNELVTRHLPPAPLFPHETPPTQSQQTQPPVAPQAPSSILLPAAPIPILSPCSPPSPQASS
LSGPSPASSRLSSSSLSSLGEDQDSVLTPEEVALCLELSEGEETPRNSVSPMPRAPSPPTTY
GYISVPTASEFTDMGRTGGVGPKGGVLLCPRPCLTPTPSEGSLANGWGSASEDNAASARA
SLVSSSDGSFLADAHFARALAVAVDSFGFGLEPREADCVFIDASSPPSPRDEIFLTPNLSLP
LWEWRPDWLEDMEVSHTQRLGRGMPPWPPDSQISSQRSQQLHCRMPKAGASPVDYS
```

Important features:

Transmembrane domain:

amino acids 448-467

N-glycosylation sites:

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

N-myristoylation sites.

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

Phosphotyrosine interaction domain proteins

amino acids 740-753

FIGURE 78

CTCCCACGGTGTCCAGCGCCAGA**ATGCGCTTCTGGTCTGCTATGGGTTGCC**TGCTGCT
CCCAGGTTATGAAGCCCTGGAGGGCCCAGAGGAATCAGCGGTTCGAAGGGACACTGTGT
CCCTGCAGTGCACCTACAGGAAGAGCTGAGGGACCACCGAAGTACTGGTGCAGGAAGGGT
GGGATCCTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAAGGCAGGAGACAAT
GAAGGGCAGGGTGTCCATCCGTGACAGCCAGGAGCTCTGCTCATTGTGACCCCTGTGGA
ACCTCACCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG
TCTTACTGATCTCTGTTGCTTCCAGGACCCCTGCTGCTCCTCCCTCCCTC
CTTCCAGCCTCTGGCTACAACACGCCTGCAAGCCAAAGGCAAAAGCTCAGCAAACCCAGCCCC
CAGGATTGACTTCTCCTGGCTCTACCCGGCAGCCACACAGCCAAGCAGGGAAAGACAGGG
GCTGAGGCCCTCCATTGCCAGGGACTTCCCAGTACGGCACGAAAGGACTCTCAGTACAC
AGGAACCTCTCCTCACCCAGCGACCTCTCCTCGCAGGGAGCTCCGCC
TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG
GTGTCCATCCCGATGGTCCGCATACTGCCAGTCCTGGTGTGCTGAGCCTTGTGAGC
CGCAGGCCTGATGCCCTCTGCAGCCACCTGCTCTGGAGAAAGGAAGCTCAACAGGCCA
CGGAGACACAGAGGAACGAGAAAGTTCTGGCTCTCAGCTGACTGCGGAGGAAAAGGAAGCC
CCTTCCCAGGCCCTGAGGGGACGTGATCTCGATGCCCTCCACACATCTGAGGAGGA
GCTGGCTCTCGAAGTTGTCTCAGCGT**AGGGCAGGAGGCC**CTCTGGCCAGGCCAGCAGT
GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTCCACCTCAGCCTCAGAG
TCCAGCTGCCCGACTCCAGGGCTCTCCCCACCCCTCCCCAGGCTCTCCTTGCATGTTCCA
GCCTGACCTAGAACGTTGTGAGCCCTGGAGGCCAGAGCGGTGCC
GAGACTGGACATCCCTGATAGGTTCACATCCCTGGCAGAGTACCAAGGCTGCTGACCCCTCA
GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTCAATCTGCCAGGA
CTCATGCCAGTGTGAGCCCTGCCTCCTCCACTCCAGACCCACCTGTCTTCCCTCCC
TGGCGCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTATGAAGAGGAGCATGCT
GGGGTGA
GACTCTGAATTCTAACAA
ATGAACGCTCACACCCCTCAGCTTAGAGTCTGCATTTGGGCTGTGACGTCTCCACCTGCC
CAATAGATCTGCTCTGCGACACCAGATCCACGTGGGACTCCCTGAGGCC
TCCAGGCCTGGTCAGGTGCACATTGCAGGATAAGCCCAGGACGGC
TTGCCTTNCCATTGCCCTCCCTGGNCCATGCC
AAACCTTGGCTCCTTGTCTGGAAAGGTTACTGCCTATGGGTTCTGGTGGCTAGAGA
GAAAAGTAGAAAACCAGAGTCAGTGCAGTGGTCTAACACAGAGGAGAGTAGGAACAGGGCGG
ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGT
GCACAACTACTATTTTTCTTTCCATTATTATTGTTTTAAGACAGAATCTGTGCT
GCTGCCAGGCTGGAGTGCAGTGGCACGATCTGCAA
CTTCTGCCTCAGCCTCCGAGTAGCTGGATTACAGGCACGC
TTC
CTCAAATGAGCCTCTGCTTCAGTCTCCAAATTGCCGGATTACAGGC
TCTGCCCTATTCCTTAAAAGTGA
ATGGAGGAGAAAAGAAAAGGAAGAAAAAATGT
TATTCGTTTGTGACTCCCTCCACTCTTCTTCTC
TTTACAGAGCAATTATCTGTATATACA
ATC
GCTGCATAAAAAAAAAAAA

FIGURE 79

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196
<subunit 1 of 1, 332 aa, 1 stop
<MW: 36143, pI: 5.89, NX(S/T): 1
MRLLVLLWGCLLPGYEALEGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIYAAEEGQETMKGRVSIRDSRQELSLIVTLWNLTQDAGEYWCVEKRGPDSSLISLFV
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPG
TSQYGHERTSQYTGTSPHPATSPPAGSSRPPMQLDSTSaedTSPALSSGSSKPRVSIPMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQTETQRNEKFWLRLTAEEKEAPSQAPEGD
VISMPPLHTSEEELGFSKFVSA
```

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128

FIGURE 80

TTGTGACTAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCAGGGGTGGCAGGA
GCCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACAGTGGTCTC
GCTCTGTTGCCAGGCTAGAGTGTACTGGCGTGTACATAGCTCACTGCAGCCTCAGACTCCT
GGACTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGACTCCAGGGGTGCACTC
GCCCTGTTCTCTCCTCTGTGAGTGGACCACGGAGGCTGGTGAGCTGCCTGTCACTCCAA
AGCTCAGCTCTGAGCCAGAGTGGTGGCTCCACCTCTGCCGCCGGCATAGAACAGGAG
CAGGGCTCTCAGAAGGCAGGTGGTGGCCAGCTGGATCATGTTGTTGGCCCTGGTCTGTCTGC
TCAGCTGCCTGCTACCCCTCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTG
CTACATGACTTCGGCTGGACGGATACGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGC
TTATTCACAAGCGGTTCAACGCAGCTGCTTGGACTACGAGGCTGATGGGAGCACCAACA
ACGGGATCTTCCAGATCAACAGCCGGAGGTGGTGCAGCAACCTCACCCCGAACGTCCCCAAC
GTGTGCCGGATGTACTGCTCAGATTGTTGAATCTAATCTCAAGGATACCGTTATCTGTGC
CATGAAGATAACCCAAGAGCCTCAGGGTCTGGTTACTGGGAGGCCTGGAGGCATCACTGCC
AGGGAAAAGACCTCACTGAATGGGTGGATGGCTGTGACTTCAGGATGGACGGAACCATGCA
CAGCAGGCTGGAAATGTGGTTGGTCTGACCTAGGCTTGGGAAGACAAGCCAGCGAATA
AAGGATGGTTAACGTGAAA

FIGURE 81

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52187
<subunit 1 of 1, 146 aa, 1 stop
<MW: 16430, pI: 5.05, NX(S/T): 1
MLLALVCLLSCLLPSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALD
YEADGSTNNGIFQINSRRWCSNLTPNVPNVCRMYSIDLNPNLKDTVICAMKITQEPQGLGY
WEAWRHHCQGKDLTEWVDGCDF
```

Important features:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 67-72

Homologous region to Alpha-lactalbumin / lysozyme C proteins.

amino acids 34-58 (catalytic domain), 111-132 and 66-107

FIGURE 82

AGCCGCTGCCCGGGCGCCCGCGCGCACCATGAGTCCCCGCTCGCCTGCGTTC
GCTGCGCCTCCTCGTCTCGCCGTCTCAGCCGCCGAGCAACTGGCTGTACCTGGCA
AGCTGTCGTGGTGGGAGCATCTCAGAGGAGGAGACGTGCGAGAAACTCAAGGGCTGATC
CAGAGGCAGGTGCAGATGTGCAAGCGAACCTGGAAGTCATGGACTCGGTGCGCCGCGTGC
CCAGCTGCCATTGAGGAGTGCCAGTACCAAGTCCGGAACCGCGCTGGAACTGCTCCACAC
TCGACTCCTGCCGTCTCGGCAAGGTGGTACGCAAGGGACTCGGGAGGCGGCCTCGTG
TACGCCATCTTCGGCAGGTGTGGCCTTGCAGTGACGCGGGCGTGCAGCAGTGGGAGCT
GGAGAAGTGCAGCTGTGACAGGACAGTGCATGGGTCAGCCCACAGGGCTTCAGTGGTCAG
GATGCTCTGACAACATCGCCTACGGTGTGGCCTCTCACAGTCGTTGTGGATGTGCGGGAG
AGAAGCAAGGGGCCTCGTCCAGCAGGCCCTCATGAACCTCCACAACAATGAGGCCGGAG
GAAGGCCATCCTGACACACATGCGGTGGAATGCAAGTGCCACGGGTGTCAGGCTCCTGTG
AGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCCGCCAGGTGGTCACGCACTGAAGGAG
AAGTTGATGGTGCACACTGAGGTGGAGCCACGCCGCGTGGCTCCTCCAGGGCACTGGTACC
ACGCAACGCACAGTTCAAGCCGACACAGATGAGGACCTGGTGTACTGGAGCCTAGCCCCG
ACTTCTGTGAGCAGGACATGCGCAGCGCGTGTGGCACGAGGGCCGCACATGCAACAAG
ACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGGCCGGCTTCCACACGGCGCA
GGTGGAGCTGGCTGAACGCTGCAGCTGCAAATTCCACTGGTGTGCTCGTCAAGTGCCGGC
AGTGCCAGCGGCTCGTGGAGTTGCACACGTGCCATGACCGCTGCCTAGCCCTGCCGGC
AACACCTAGTGGCCAGGGAAGGCCATAATTAAACAGTCTCCCACCACTACCCAAGA
GATACTGGTTGTATTTTGTCTGGTTGGTTGGTCTCATGTTATTATTGCCGAA
ACCAGGCAGGCAACCCAAGGGCACCAACCAGGGCTCCCAAAGCCTGGGCTTGTGGCT
GCCACTGACCAAGGGACCTTGCTCGTGCCGCTGGCTGCCGATGTGGCTGCCACTGACCA
CTCAGTTGTATCTGTGTCGTTCTACTTGCAAGACCTAACGGTGGAGTAACAAGGAGTAT
TACCACACATGGCTACTGACCGTGTACGGGAAGAGGGGCTTATGGCAGGGAAAATA
GGTACCGACTTGATGGAAGTCACACCTCTGGAAAAAAAGAACTCTTAACCTCCAGCACACA
TACACATGGACTCCTGGCAGCTTGAGCCTAGAACGCATGTCTCTCAAATGCCCTGAGAAAGG
GAACAAGCAGATACCAGGTCAAGGGCACCAAGGTTCATTCAGCCCTACATGGACAGCTAGA
GGTCGATATCTGTGGTCCTCCAGGCAAGAAGAGGGAGATGAGAGCAAGAGACGACTGAA
GTCCCACCCCTAGAACCCAGCCTGCCAGCCTGCCCTGGGAAGAGGAAACTTAACCACTCC
CCAGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACCAGGGATCCGGCTGTGCCCT
TGCAGTCATGCCGAGTCACCTTCACAGCGCTGTTCCATGAAACTGAAAAACACACAC
AC
GAGAGGGAGGAAAGGGCTGTGCCTTGCAGTCATGCCGAGTCACCTTCACAGCACTGTCCTC

FIGURE 83

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328
<subunit 1 of 1, 351 aa, 1 stop
<MW: 39052, pI: 8.97, NX(S/T): 2
MSPRSCLRSLRLLVFAVFSAAASNWLAKLSSVGSISEEETCEKLKGLIQRQVQMCKRNL
VMDSVRRGAQLAIEECQYQFRNRRWCSTLDSLPVFGKVTQGTREAAFVYAISSAGVAFAV
TRACSSGELEKCGCDRTVHGVPQGFQWSGCSDNIAYGVAFSQSFDVRERSKGASSSRLM
NLHNNEAGRKAILETHMRVECKCHGVSGSCEVKTCWRRAVPPFRQVGHALKEKFDGATEVEPR
VGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTSKAIDGCELLC
CGRGFHTAQVELAERCSCKFHWCCFVKCQCQRLVELHTCR
```

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 88-91 and 297-300

Wnt-1 family signature.

amino acids 206-215

Homologous region to Wnt-1 family proteins

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

FIGURE 84

CGGACGCGTGGCGGACGCGTGGCGGACGCGTGGCGGACGCGTGGCTGGTGCCTGCAT
CGCCATGGACACCACCAAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGGAGGGC
CCTGGGGACGCTGGTGCACGGAGCAGGAGACCCCTTTCTGGCCCTGGCTGTCTGGTC
ACCACAGTCCTTGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGC
GGCGCTGCTTGACGCCACGACCTGCTGAGGACAAACGCCCTGAAGCAGACGGCGCTGG
GTGCCCTGAAGGAGGAGGTGGAGACTGCCACAGCTGCTGGGGACGCAGGCGCAGCTG
CAGACCACGCCCGGGAGCTTGGGAGGCCAGCGAAGCTGATGGAGCAGGAGAGCGCCCT
GCGGGAACTGCGTGAGCGCGTGACCCAGGGCTGGCTGAAGCCGGCAGGGCCGTGAGGACG
TCCGCACTGAGCTGTTCCGGCGCTGGAGGCCGTGAGGCTCCAGAACAAACTCCTGCGAGCCG
TGCCCCACGTCGTGGCTGTCCTCGAGGGCTCTGCTACTTTCTGTGCCAAAGACGAC
GTGGGCGGCGGCAGGATCACTGCGCAGATGCCAGCGCACCTGGTATCGTTGGGGCC
TGGATGAGCAGGGCTTCCTCACTCGAACACGCGTGGCGTGGTTACTGGCTGGCGTGGAGG
GCTGTGCGCCATCTGGCAAGGTTAGGGCTACCACTGGGTGGACGGAGTCTCTCAGCTT
CAGCCACTGGAACCAGGGAGAGGCCAATGACGCTGGGGCGCGAGAACTGTGTCATGATGC
TGCACACGGGCTGTGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAG
AAAAGGCACAACTGTGACCCGCCAGTGCCTGGAGGCCGCATTGCAGCATGCGTA
TCCTGGGGCTGCTCACCTCCCTGGCTCTGGAGCTGATTGCCAAAGAGTTTTTCTTCCT
CATCCACCGCTGCTGAGTCTCAGAAACACTGGCCAACATAGCCCTGTCCAGCCCAGTGC
TGGGCTCTGGACCTCCATGCCGACCTCATCTTAACCTCACGCAGACCCAACCTAAC
TCCACTAGCTCCAAAATCCCTGCTCCTGCGTCCCGTGAATATGCCTCCACTCTCCCTAA
CCAAGGTTAGGTGACTGAGGACTGGAGCTGTTGGCTTCGCATTTCCACCAAACGG
AGCTGTTTGCGAGCTGAGGAAGCATCAATAATTTGAGAAATGAAAAAA

FIGURE 85

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352
<subunit 1 of 1, 293 aa, 1 stop
<MW: 32562, pI: 6.53, NX(S/T): 2
MDTTRYSKWGGSEEVPGGPWGRWVHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAA
LLDGHDLLRTNASKQTAALGALKEEVGDCHSCCSGTQAQLQTTRAELGEAQAKLMEQESALR
ELRERVTQGLAEAGRGRGREDVRTELFRALLEAVRLQNNSCEPCPSTSWSFEGSCYFFSVPKTTW
AAAQDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLFS
HWNQGEPNDAWGRENCSVMMLHTGLWNDAPCDSEKDGWICEKRHNC
```

Important features:

Type II transmembrane domain:

amino acids 31-54

N-glycosylation sites.

amino acids 73-76 and 159-162

Leucine zipper pattern.

amino acids 102-123

N-myristoylation sites.

amino acids 18-23, 133-138 and 242-247

C-type lectin domain signature.

amino acids 264-287

FIGURE 86

GCCAGGGGAAGAGGGTATCCGACCCGGGGAGGTCGCTGGCAGGGCGAGTTGGAAAGCG
GCAGCCCCCGCCGCCCGCAGCCCCTCTCCTCCTTCTCCACGTCTATCTGCCTCTCG
CTGGAGGCCAGGCCGTGCAGCATCGAAGACAGGAGGAACCTGGAGCCTCATTGGCGGCCGG
GGCGCCGGCCTCGGGCTTAAATAGGAGCTCCGGCTCTGGCTGGACCCGACCGCTGCCGG
CGCGCTCCGCTGCTCTGCCGGGTGATGGAAAACCCCAGCCGGCGCCGCCCTGGCAAG
GCCCTCTGCGCTCTCCTGGCCACTCTCGCGCCGCCAGCCTCTTGGGAGAGTC
CATCTGTTCCGCCAGAGCCCCGCCAAATACAGCATCACCTCACGGCAAGTGGAGCCAGA
CGGCCTTCCCCAAGCAGTACCCCTGTTCCGCCCTGCGCAGTGGTCTCGCTGCTGGGG
GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACAGTACGTCACTAACGGCTGCG
CGACTTGCAGCGGGCAGGCGCTGGCGTGTAGAAGGAGATCGAGGCGGGAGGAGG
CGCTGCAGAGCGTGCACGAGGTGTTTGGCGCCGCTCCAGCGGCACCGGGCAGACG
TCGGCGGAGCTGGAGGTGCAGCGCAGGCACTCGCTGGTCTCGTTGTGGTGCATCGGCC
CAGCCCCGACTGGTCTGGCGTGGACAGCCTGGACCTGTGCGACGGGACCGGGCTCACCTCTCC
AACAGGCGGCCTGGACCTGTACCCCTACGACGCCGGACGGACAGCGGCTCACCTCTCC
TCCCCCAACTCGCCACCATCCCGAGGACACGGTACCGAGATAACGTCCCTCTCCAG
CCACCCGGCCAACCTCCTCTACTACCCGGCTGAAGGCCCTGCCTCCATGCCAGGGTGA
CACTGCTGCCGTGCGACAGAGCCCCAGGGCCTCATCCCTCCGCCAGTCCTGCCAGC
AGGGACAATGAGATTGTAGACAGCGCCTCAGTTCAAGAACGCCGCTGGACTGCGAGGTCTC
CCTGTGGTCTGGGACTGTGGAGGCCACTGTGGAGGCTGGACCAAGAGCAGGA
CTCGCTACGTCCGGTCCAGCCGCCAACACGGGAGGCCCTGCCAGCTCGAAGAAGAG
GCTGAGTGCCTGATAACTGCGTCTAAAGACCAGAGCCCCGAGCCCTGGGGCCCCCG
GAGCCATGGGTGTCGGGGCTCTGTGCAGGCTCATGCTGCAGGGGCCAGGGCACAGGG
GGTTTGCCTGCTGGGACTGTGGAGGCCACTGTGGAGGCTGGACCAAGAGGCCCT
CTGGTGGCCGGCACGGCATTGGAAACAGCCTCCTTCCAACCTTGCTTCTAGGGG
CCCCCGTGTCCGTCTGCTCTAGCCTCCTGCAGGATAAGTCATCCCCAAGGCTC
CAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGCTGCTCCAGGAGATTGCTTCTCG
TCCAGGGGCCTGGCTCCACGTGGTGCAGATACTCAGACCTGGTGCTCTAGGCTGTGCTG
AGCCCACCTCCCGAGGGCGCATCCAAGCGGGGCCACTTGAGAAGTGAATAAAATGGGGCG
TTTCGGAAGCGTCAGTGTTCATGTTATGGATCTCTGCCTTGAATAAAAGACTATCTCT
GTTGCTCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

Q
S
H
M
D
S
W
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G
H

FIGURE 87

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53971
><subunit 1 of 1, 331 aa, 1 stop
><MW: 35844, pI: 5.45, NX(S/T): 2
MENPSPAAALGKALCALLLATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPL
FRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAERGEAWALMKEIEAAGEALQSVHEVF
SAPAVPSGTGQTSAELEVQRRHSLVSFVVRIVPSPDWFVGVDSDLLCDGDRWREQAALDLYP
YDAGTDGFTFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLLRLRQSP
RAFIPPPAPVLPSPRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGRLGKSRTRYVRVQPA
NNGSPCPELEEEAECVPDNCV
```

Important features:

Signal peptide:

amino acids 1-26

FIGURE 88

GGCGGGGTCCGTGAGGGGCTCCTTGGCAGGGTAGTGTGTTGGTGTCCCTGTCTGCGTGA
TATTGACAAACTGAAGCTTCCTGCACCACTGGACTTAAGGAAGAGTGTACTCGTAGGCCGA
CAGCTTAGTGGCCGGCGGCCGCTCTCATCCCCGTAAGGAGCAGAGTCCTTGTACTGAC
CAAGATGAGCAACATCTACATCCAGGAGCCTCCCACGAATGGAAAGGTTTATTGAAAACTA
CAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTGAGAAATT
ATCCAACTTGTTGGAAGCTTATTATGACAATACCATTTCATAGAGTTGTGCCTGGTTT
CATAGTCCAAGGCGGAGATCCTACTGGCACAGGGAGTGGAGAGTCTATCTATGGAGCGC
CATTCAAAGATGAATTTCATTACGGTTGCGTTTAATCGGAGAGGACTGGTGCATGGCA
AATGCTGGTTCTCATGATAATGGCAGCCAGTTTCTTACACTGGTCGAGCAGATGA
TAACAATAAGCATACCCTTGAAAGGTTACAGGGATACTGAGTATATAACATGTTGCAC
TGTCAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAATAAAAGCTGT
GAGGTTTGTAAATCCTTTGATGACATCATTCCAAGGGAAATTAAAAGGCTGAAAAAAGA
GAAACCAGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAAATTAGTTACTTT
CATTGGAGAGGAAGCTGAGGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAG
GGCAAAAGCAAAAGTAGTCATGACTTGCTTAAGGATGATCCACATCTCAGTTCTGTTCCAGT
TGTAGAAAGTAAAAAGGTGATGCACCAAGATTAGTTGATGATGGAGAAGATGAAAGTGCAG
AGCATGATGAATATATTGATGGTATGAAAAGAACCTGATGAGAGAAAGAATTGCCAAAAA
TTAAAAAAAGGACACAAGTGCATGAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATC
AGTCAGCCGCAGTGAAGAGCTCAGAAAAGCAAGACAATTAAAACGGAACTCTAGCAG
CAAAACAAAAAAAGTAGAAAATGCAGAAAACAAGCAGAAAAAGAAGTGAAGAGGAAGAA
GCCCTCCAGATGGTGTGTTGCCAATACAGAAGAGAAAAGCAAAAGTATGAAGCTTGAG
GAAGCAACAGTCAAAGAAGGAACTTCCGGAAAGATCAGACCCCTGCACTGCTGAACCAGT
TTAAATCTAAACTCACTCAAGCAATTGCTGAAACACCTGAAAATGACATTCTGAAACAGAA
GTAGAAGATGATGAAGGATGGATGTCACATGTACTTCAGTTGAGGATAAAAGCAGAAAAGT
GAAAGATGCAAGCATGCAAGACTCAGATACTTGAATCTATGATCCTCGGAATCCAGTGA
ATAAAAGAAGGAGGGAAGAAAGCAAAAGCTGATGAGAGAGAAAAAGAAAGAAGATAAAAT
GAGAATAATGATAACCAGAACTTGCTGGAAATGTGCCTACAATGGCCTGTAACAGCCATTG
TTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTGAAACCTGTTGCTGGTTTG
AAAAACAATTATCTTGTGTTGCAAATTGTGGAATGATGTAAGCAAATGCTTTGGTTACTGG
TACATGTGTTTCTAGCTGACCTTATATTGCTAAATCTGAAATAAAACTTCCCT
TCCACAAAAAA

FIGURE 89

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919
><subunit 1 of 1, 472 aa, 1 stop
><MW: 53847, pI: 5.75, NX(S/T): 2
MSNIYIYIQLCLEAYYDNTIFHRVVPGFI
VQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFTLGRADELN
NKHTIFGKVTGDTVYNMLRLSEVDIDDDERPHNPHKIKSCEVLNFNPFDIIPREIKRLKKEK
PEEEVKKLKPKGTKNFSLSFGEAEEEEEVNRVSQSMKGKSKSSHDLKDDPHLSSVPVV
ESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKLLKKDTSANVKSAGEGEVEKKSV
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEEAPPDGAVAЕYRREKQKYEALRK
QQSKKGTREDQTLALLNQFKSKLTQAIATPENDIPETEVEDDEGWMShVLQFEDKSRKVK
DASMQDSDTFeIYDPRNPVNKRREESKKLMREKKERR
```

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 109-112 and 201-204

Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.

amino acids 49-66

Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase

amino acids 96-140, 49-89 and 22-51

FIGURE 90

CGCCGCCGTTGGGGCTGGAAGTCCGCCAGGTCCGTGCCGGCGAGAGAGATGCTGCCGG
CCGCCTCGCTTGAGGCGAGAGAAGTGTCCCAGACCCATTGCCCTGCTGACGGCGTCC
AGCCCTGGCCAGACATGTCCACAGGGTCTCCTCGGGTCCGGACTCTGGCTCCACCACC
GTGGCCGCCGGCGGACCAGCACAGGCAGCGTTCTCCTCGGAACGGAACGTCTAGCAA
CCCTCTGTGGGCTCAATTGGAAATCTTGGAAAGTACTTCAACTCCAGCAACTACATCTG
CTCCTCAAGTGGTTTGGAACCGGGCTTTGGATCTAAACCTGCCACTGGGTTCACTCTA
GGAGGAACAAATACAGGTGCCTGCACACCAAGAGGCTCAAGTGGTCACAAATATGGAAC
CCTGCAAGGAAAACAGATGCATGTGGGAAGACACCCATCCAAGTCTTTAGGAGTCCCCT
TCTCCAGACCTCCTCTAGGTATCCTCAGGTTGCACCTCAGAACCCCCGGAGCCCTGGAAA
GGAATCAGAGATGCTACCACCTACCCGCCTGGATGGAGTCTCGCTCTGTCGCCAGGCTGGAG
TGCAGTGGCACGATCTGGCTCACTGCAACCTCCGCCTCCGGGTTCAAGCGAGTCTCCTGC
CTCAGCCTCTGAGTGTCTGGGCTACAGGTGCCTGCAGGAGTCTGGGCGAGCTGCCCTCG
ATGTACGTCAGCACGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACCT
GAACGTGTACGCCGGCGCGCGCCCAGGATCCCCAGCTGCCAGTGTGGCTGGTTCC
CGGGAGGCGCCTTCATCGTGGCGCTGCTTCTCGTACGAGGGCTCTGACTTGGCCCGCG
GAGAAAGTGGTGTGGTTCTGCAGCACAGGCTGGCATCTTGGCTTCTGAGCACGGA
CGACAGCCACGCCGGGAACGGGGCTGGACAGATGGCGCTCGCGCTGGGTGC
AGGAGAACATCGCAGCCTCGGGGAGACCCAGGAAATGTGACCCCTGTCGGCCAGTCGGCG
GGGGCCATGAGCATCTCAGGACTGATGATGTCACCCCTAGCCTCGGGTCTTCCATCGGGC
CATTTCCAGAGTGGCACCGCTTATTCACTAGTAACTGAAAGTGG
CCAAGAAGGTTGCCACCTGGCTGGATGCAACCACAAACAGCACACAGATCTGGTAAACTGC
CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCACAGGATGAGATTCTCTCCA
GAACCTCCAGAGAGACCCGGAAAGAGATTATCTGGTCCATGAGCCCTGTTGGATGGTGG
TGATCCCAGATGACCCCTTGGTGTCTCTGACCCAGGGGAAGGTTCATCTGTGCCCTACCTT
CTAGGTGTCAACAAACCTGGAATTCAATTGGCTCTGCCTTATAATATCACCAAGGAGCAGGT
ACCACTGTGGTGGAGGAGTACCTGGACAATGTCATGAGCATGACTGGAAAGATGCTACGAA
ACCGTATGATGGACATAGTTCAAGATGCCACTTCGTGTATGCCACACTGCAGACTGCTCAC
TACCAACCGAGAAACCCAAATGATGGGAATCTGCCCTGCTGGCACGCTACAACAAGGATGAA
AAGTACCTGCAGCTGGATTTACCAAGAGTGGCATGAAGCTCAAGGAGAAGAAGATGGC
TTTTGGATGAGTCTGTACCAAGCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGC
TATGCAGGAAGGAGCCAAAGAGGGTTGCCCTACCCAGGTTAGAAACTGCAGGAGCTCCCTGCT
TGGACATACCTGGGACAAGAGTTCTACCCACCCAGGTTAGAAACTGCAGGAGCTCCCTGCT
GCCTCCAGGCCAAAGCTAGAGCTTGTGACTCCTTCTATGGGAGGTCGACCCAGACTGCCACTGC
TGACATCCCATGATGCCCTCTACTTCACTGTTGACATCCAGTTAGGCCAGGCCCTGTCAAC
ACCACACTGTGCTCAGCTCTCCAGCCTCAGGACAACTCTTTCCCTCTCAAATCCT
CCCACCTTCAATGTCCTTGTGACTCCTTCTATGGGAGGTCGACCCAGACTGCCACTGC
CCCTGTCAGCACCAGCTTGGCATTACCATCCATCTGCTCAACCTTGTCTGTCTGT
TCACATTGGCTGGAGGCCTAGGGCAGGTTGTGACATGGAGCAAACCTTGGTAGTTGGGA
TCTTCTCTCCACCCACACTTATCTCCCCAGGGCCACTCCAAAGTCTATACACAGGGTGG
TCTCTCAATAAAGAAGTGTGATTAGAAAAAA

FIGURE 91

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179
<subunit 1 of 1, 545 aa, 1 stop
<MW: 58934, pI: 9.45, NX(S/T): 4
MSTGFSFGSGTTLGTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTTPATTSSAPSSG
FGTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTLQGKQMHVGKTPIQVFLGVPSRPP
LGILRFAPPEPPEPWKGIRDATTYPPGWSLALSPGWSAVARSRLTATSASRVQASLLPQPLS
VWGYRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLNYYAPARAPGDPQLPVMVWFPGGAF
IVGAASSYEGSDLAAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMAALRWVQENIA
AFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA
HLAGCNHNSTQILVNCLRALSGTKVMRVSNKMRFLQLNFQRDPEEIIWSMSPVVDGVVIPDD
PLVLLTQGKVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEYLDNVNEHDWKMLRNRMMD
IVQDATFVYATLQTAHYHRETPMMGICPAGHATTRMKSTCSWILPQEWA
```

Important features:

Signal peptide:

amino acids 1-29

Carboxylesterases type-B serine active site.

amino acids 312-327

Carboxylesterases type-B signature 2.

amino acids 218-228

N-glycosylation sites.

amino acids 318-321, 380-383 and 465-468

FIGURE 92

GAGAACAGGCCTGTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATGCTACTGCCACTGCT
GCTGTCCTCGCTGCTGGCGGGTCCCAGGCTATGGATGGGAGATTCTGGATACGAGTGCAGG
AGTCAGTGATGGTGCCTGGAGGGCCTGTGCATCTCTGCCCCCTGCTCTTCTCCTACCCCCGA
CAAGACTGGACAGGGTCTACCCAGCTATGGCTACTGGTTCAAAGCAGTGACTGAGACAAAC
CAAGGGTGCCTGTGCCACAAACCACCAAGAGTCGAGAGGTGGAAATGAGCACCCGGGGCC
GATTCCAGCTCACTGGGGATCCGCCAACGGGAACGTGCTCCTGGTGCAGAGACGCGCAG
ATGCAGGATGAGTCACAGTACTCTTCGGGTGGAGAGAGGAAGCTATGTGACATATAATT
CATGAACGATGGGTTCTTCTAAAGTAACAGTGCTCAGCTCACGCCAGACCCAGGACC
ACAACACCGACCTCACCTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACC
GTCCGACTCCGTGTGGCTATGCCAGAGACCTTGTATCAGCATTACGTGACAACAC
GCCAGCCCTGGAGCCCCAGCCAGGGAAATGTCCACACTGGAAAGGCCAAAAAGGCCAGT
TCCTGCGGCTCCTCTGTGCTGACAGCCAGCCCCCTGCCACACTGAGCTGGTCTGCAG
AACAGAGTCTCTCCTCGTCCCATCCCTGGGCCCTAGACCCCTGGGCTGGAGCTGCCGG
GGTGAAGGCTGGGATTCAAGGGCGCTACACCTGCCAGCGGAGAACAGGCTGGCTCCAGC
AGCGAGCCCTGGACCTCTGTGCACTATCCTCCAGAGAACCTGAGAGTGATGGTTCCCAA
GCAAAACAGGACAGTCCTGGAAAACCTTGGAACGGCACGTCTCTCCAGTACTGGAGGGCCA
AAGCCTGTGCCCTGGTCTGTGTCACACACAGCAGCCCCCAGCCAGGCTGAGCTGGACCCAGA
GGGGACAGGTTCTGAGCCCCCTCCAGCCCTCAGACCCCGGGCTCTGGAGCTGCCTGGGTT
CAAGTGGAGCACGAAGGAGAGTTCACCTGCCACGCTCGGACCCACTGGCTCCAGCACGT
CTCTCTCAGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGATTCTCCAACGGAG
CGTTCTGGGAATCGGCATCACGGCTCTCTTCTCTGCCCTGATCATCATGAAG
ATTCTACCGAAGAGACGGACTCAGACAGAAACCCCGAGGCCAGGTTCTCCGGCACAGCAC
GATCCTGGATTACATCAATGTGGTCCCAGCCCTGGCTCAGAAGCGGAATCAGA
AAGCCACACAAACAGTCCTCGGACCCCTCCTCACCAGGTGCTCCCTCCCCAGAATCAAAG
AAGAACCAAGAAAAGCAGTATCAGTTGCCAGTTCCCAGAACCCAAATCATCCACTCAAGC
CCCAGAATCCCAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTCCCAGGCGTCA
GACCCAGGCTGAGGCCGGATGCCAACGGCACCCAGGGATTATGAGAACAGTCAAGTTC
CAATGAAGGGTCTCTTAGGCTTTAGGACTGGACTTCGGCTAGGGAGGAAGGTAGAGTAAGAG
GTTGAAGATAACAGAGTGCAAAGTTCTCTCTCCCTCTCTCTCTCTCTCTCTCTCT
CT
CCAGCACTTGGGAGGGTGGAGGTGAGGTGGGAGATCGCCTGAGGTGGAGTTGGAGACCCAGCCTG
GCCAACTTGGTGAACCCCGTCTACTAAAAATACAAAAATTAGCTGGCATGGTGGCAGG
CGCCTGTAATCCTACCTACTTGGGAAGCTGAGGCAGGAGAACACTGAACCTGGGAGACGG
AGGTTGCAGTGAGCCAAGATCACACCATTGCACGCCAGCCTGGCAACAAAGCAGAGACTCCA
TCTCAAAAAAAATCCTCAAATGGGTGGGTCTGTAATCCAGCACTTGGGAGGCTA
AGGTGGGTGGATTGCTTGAGGCCAGGAGTTGAGACCCAGCAGCTGGCAACATGGTAAACCC
ATCTCTACAAAAAATACAAAACATAGCTGGCTTGGTGTGCTGTAGTCCAGCTGT
CAGACATTAAACAGAGCAACTCCATCTGAATAGGAGCTGAATAAAATGAGGCTGAGACC
TACTGGGCTGCATTCTCAGACAGTGGAGGCATTCTAAGTCACAGGATGAGACAGGAGGTCCG
TACAAGATAACAGGTATAAAGACTTGTGATAAAACAGATTGAGTAAAGAAGCCAACCAA
ATCCCACCAAAACCAAGTTGCCACGAGAGTGACCTCTGGTCGTCTCACTGCTACACTCCT
GACAGCACCAGACAGTTACAAATGCCATGGCAACATCAGGAAGTTACCGATATGTCCCA
AAAGGGGGAGGAATGAATAATCCACCCCTGTTAGCAAATAAGCAAGAAATAACCATAAAA
GTGGGCAACCAGCAGCTCTAGGCCTGCTCTGTATGGAGTAGCCATTCTTGTCTT
TACTTCTTAATAAACTGCTTCACTTAAAAAA

FIGURE 93

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002
><subunit 1 of 1, 544 aa, 1 stop
><MW: 60268, pI: 9.53, NX(S/T): 3
MLLPLLLSSLLGGSQAMDGRFWIRVQESVMPEGLCISVPCSFSYPRQDWGSTPAYGYWFK
AVTETTKGAPVATNHQSREVMSTRGRFQLTGDPAKGNCSL VIRDAQM QDESQYFFRVERGS
YVTYNFMNDGFFLKVTVLSFTPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVIS
ISRDNTPALEPQPQGNVPYLEAQKGQFLRLCAADSQPPATLSWVLQNRVLSSHPWGPRPL
GLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENLNGNTSL
PVLEGQSLCLVCVTHSSPPARLSWTQRGQLSPSQPSDPGVLELPRVQVEHEGEFTCHARHP
LGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPR
FSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPPPGAPSPESKKNQKKQYQLPSFPEP
KSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ
```

Important features:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 100-103, 297-300 and 306-309

Immunoglobulins and major histocompatibility complex proteins signature.

amino acids 365-371

FIGURE 94

TGAAGAGTAATAGTTGGAATCAAAAGAGTCACCGCAATGAACTGTTATTTACTGCTGCGTTT
TATGTTGGATTCCCTCTCATGGCCTGCTGGAGCAACAGAAAACTCTCAAACAAAGA
AAGTCAGCAGCCAGTGCATCTCATTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATT
TTTGTACCAAGAGGAATGAATACGACTAGTCATCACATCGGCCAGCTAAGATCTGATTAGA
CAATGGAAACAATTCTTCCAGTACAAGCTTGGGAGCTGGAGCTGGAAAGTACTTTATCA
TTGATGAAAGAACAGGTGACATATGCCATACAGAAGCTGATAGAGAGGAGCGATCCCTC
TACATCTTAAGAGGCCAGGTAAAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGA
GTTTGTCAAAAGTTCGGATATCAATGACAATGAACCAAATTCTTAGATGAACCTTATG
AGGCCATTGTACCAAGAGATGTCAGAGAACATTAGTTATCCAGGTGACAGCAAGTGAT
GCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCTACAGCTACTTCAAGGCCAGCC
ATATTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTCTAAAATGGATAGAGAAC
TGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG
TCTGGAAACAACAAGTGTATTAACTTCAGATGTTAATGACAATAAGCCTATATTAA
AGAAAGTTTATACCGCTGACTGTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA
TCATGGCATATGATAATGACATAGGAGAGAATGCAAGAAATGGATTACAGCATTGAAGAGGAT
GATTGCAAACATTGACATTACTAATCATGAAACTCAAGAAGGAATAGTTATTTAA
AAAGAAAGTGGATTGAGCACCAGAACACTACGGTATTAGAGCAAAAGTTAAAACCATC
ATGTTCTGAGCAGCTCATGAAGTACCAACTGAGGCTTCCACCTTCAAGATCCAG
GTGGAAGATGTTGATGAGCCTCCTCTTCCCTCCATATTATGTTGAAGTTTTGA
AGAAACCCCACAGGGATCATTGTAGGCGTGGTGTGCCACAGACCCAGACAATAGGAAT
CTCCTATCAGGTATTCTATTACTAGGAGCAAAGTGTCAATATCAATGATAATGGTACAATC
ACTACAAGTAACACTGGATCGVAAATCAGTGCTGGTACAACCTAAGTATTACAGCCAC
AGAAAAATACAATATAGAACAGATCTCTCGATCCCACGTGATGCAAGTTCTAACATCA
ATGATCATGCTCCTGAGTTCTCTCAATAACTATGAGACTTATGTTGTGAAATGCAGGCTCT
GGTCAGGTAATTCAAGACTATCAGTGAGGATAGAGATGAATCCATAGAACAGCACCATT
TTACTTTAATCTATCTGAGAACACTAACATTCAAGTTACAATCATAGATAATCAAG
ATAAACACAGCTGTCATTGACTAATAGAACACTGGTTAACCTCAAGAACAGACCTGCTTC
TACATCTCCATCTTAATTGCCGACAATGAAATCCGTCACTTACAAGTACAACACCCTTAC
CATCCATGTCGTGACTGTGGTACAGTGGAGCACACAGACCTGCCAGTACCAAGGAGCTTG
TGCTTCCATGGGATTCAAGACAGAACAGTTATCATTGCTATTCTCATTGCAATTGATCATA
TTTGGGTTTATTTTGACTTTGGTTAAAACACAGGAGAAAACAGATTCTATTCTGA
GAAAAGTGAAGATTCAAGAGAACATATTCAATATGATGATGAAGGGGTGGAGAACAG
ATACAGAGGCCTTGATATAGCAGAGCTGAGGAGTAGTACCATATGCCAGTGGCCCCGA
CGGAAAACCACAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTGCAAGTTGGCCCCGA
CAGTGCCATATTCAAGAACATTCTGGAAAAGCTCGAAGAACGCTAATACTGATCCGTGTG
CCCCCTCTTGTGATTCCCTCCAGACCTACGCTTGGAGGGAACAGGGCATTAGCTGGATCC
CTGAGCTCCTTAGAATCAGCAGTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTT
GGGACCTCGCTTAAAAGATTAGCATGCATGTTGGTCTGCAGTGCAAGTCAAATAATTAGG
GCTTTTACCATCAAAATTAAAAGTCTAATGTTGATTCGAACCAATGGTAGTCTTAA
AGAGTTTGTCGCCCTGGCTCATGGGGAAAGCCCTAGTCTATGGAGTTCTGATTCC
CTGGAGTAAATACTCCATGGTTATTTAAGCTACCTACATGCTGTCAATTGAAACAGAGATGTG
GGGAGAACATGAAACAAATCAGCTCACAGGCATCAATACAACCAGATTGAAGTAAAATAATG
TAGGAAGATATTAAAAGTAGATGAGAGGACACAAGATGAGTCGATCCTTATGCGATTATAT
CATTATTACTTAGGAAAGAGTAAAATACCAACAGGAGAAAATTAAAGGAGCAAAATTG
CAAGTCAAATAGAAATGTACAAATCGAGATAACATTACATTCTATCATATTGACATGAAA
ATTGAAAATGTATAGTCAGAGAAATTTCATGAATTATTCCATGAAGTATTGTTCTTAT
TTAAA

FIGURE 95

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906
><subunit 1 of 1, 772 aa, 1 stop
><MW: 87002, pI: 4.64, NX(S/T): 8
MNCYLLLRFMLGIPLLWPCLGATENSQTKVKQPVRSHLRVKRGWVWNQFFVPEEMNTTSHH
IGQLRSLDNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT
GRAVEPESEFVIKVSDINDNEPKFLDEPYEAIPEMSPEGLVVIQVTASDADDPSSGNARL
LYSLLQGQPYFSVEPTGVIRISSLKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLSD
VNDNKPIFKESLYRLTVSESAPGTTSIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE
TQEGIVILKKVDFEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLL
PYYVFEVFEETPQGSFVGVVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISA
WYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDR
DESIEHHFYFNLSVEDTNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIAADNGIP
SLTSTNTLTIHVCDCGDGSQTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTGLKQ
RRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY
RQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDLQTYAFEGTGSLAGSLSLESAVSDQD
ESYDYLNELGPRFKRLACMFGSAVQSNN
```

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 597-617

N-glycosylation sites.

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,
516-519 and 534-537

Cadherins extracellular repeated domain signature.

amino acids 136-146 and 244-254

FIGURE 96

ATTTCAAGGCCAGCCATATTTNTGTTAACCAACAACAGGAGTCATAAGAATATTTNTA
AAATGGATAGAGAACTGCAAGATGAGTATTGGGTAAATCATTCAAGCCAAGGACATGATTGGT
CAGCCAGGAGCGTTGTNTGGAACAACAAGTGTATTAATTAAACTTCAGATGTTAATGACAA
TAAGCCTATATTTAAAGAAAGTTATACCGCTTGAUTGTNTNTGAATCTGCACCCACTGGGA
NTTNTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTAC
AGCATTGAAGAGGGATGATTGCAAACATTGACATTATT

FIGURE 97

GCAACCTCAGCTCTAGTATCCAGACTCCAGCGCCGCCGGCGCGAACCCAAACCCGAC
CCAGAGCTTCTCCAGCGGCGCAGCGAGCAGGGCTCCCGCTTAACCTCCTCCGGGG
CCCAGCCACCTCGGGAGTCGGGTTGCCACCTGCAAACCTCCGCCTCTGCACCTGCCA
CCCCTGAGCCAGCGCGGCCCGAGCGAGTCATGGCCAACGCCGGCTCAGCTGGAG
TTCATTCTCGCCTCTGGGATGGATCGGCGCCATCGTCACTGCCCTGCCAGTGGAG
GATTACTCCTATGCCGGGACAACATCGTGACCGGCCAGGCCATGTACGAGGGCTGTGGA
TGTCTCGGTGCGAGAGCACCAGGAGATCCAGTGCAAAGTCTTGACTCCTGCTGAAT
CTGAGCAGCACATTGCAAGCAACCGTGCTTGATGGTGGCATCCTCTGGAGTGAT
AGCAATCTTGTGGCCACCCTGGCATGAAGTGTATGAAGTGCTTGAAGACGATGAGGTGC
AGAAGATGAGGATGGCTGTCAATTGGGGTGCATATTCTTCTTGAGGTCTGGCTATT
GTTGCCACAGCATGGTATGCAATAGAATCGTCAAGAATTCTATGACCCATGACCCAGT
CAATGCCAGGTACGAATTGGTCAGGCTCTCACTGGCTGGCTGCTGCTCTGCC
TTCTGGGAGGTGCCCTACTTGCTGTCTGTCCCCGAAAAACAAACCTCTACCCAAACACCA
AGGCCCTATCCAAAACCTGCACCTCCAGCGGGAAAGACTACGTGTGACCACAGAGGCAAAAG
GAGAAAATCATGTTGAAACAAACGAAAATGGACATTGAGATACTATCATTAAACATTAGGAC
CTTAGAATTGGGTATTGTAATCTGAAGTATGGTATTACAAAACAAACAAACAAACAAAAA
ACCCATGTGTTAAATACTCAGTCTAAACATGGCTTAATCTTATTGTTATCTTCTTC
ATATAGGAGGGAAGATTTCATTGTATTACTGCTCCATTGAGTAATCATACTCAAAT
GGGGGAAGGGGTGCTCTTAAATATATAGATATGTATATACATGTTTCTATTAAAAA
ATAGACAGTAAAATACTATTCTCATTATGTTGATACTAGCATACTTAAATATCTCTAAAAT
AGGTAATGTATTAAATTCCATTGATGAAGATGTTATTGGTATATTCTTCTTC
TTATATACATATGTAACAGTCAAATATCATTACTCTCTCATTAGCTTGGGTGCCTTG
CCACAAGACTAGCCTAATTACCAAGGATGAATTCTTCAATTCTCATGCGTGCCTT
CATATACTTATTAAATTGTTACCATATCTTACGACTTGCACTGCTTATTAGCCTT
TTGTTTGTGTTCTATTGGCTCTATCCTGAATCTAACACATTCTAGCCTACATT
GTTCTAAAGCCAAGAAGAATTATTACAAATCAGAACTTGGAGGCAAATCTTCTGCATG
ACCAAAGTGATAAATTCTGTTGACCTCCCACACAATCCCTGACTCTGACCCATAGCACT
CTGTTGCTTGAAGAATATTGCAATTGAGTAGCTGCATGCTGTTCCCCAGGTGTTG
AACACAACCTTATTGATTGAAATTGAGCTACTTATTGATGTTTATATCCCCCTAAACT
ACCTTTGTTCTCCCATTCTTAATTGTTATTGAGCTACTTATTGATGTTTATATCTT
TATCTTCTTAATAAGGTGTTGCTGTTGCTGAACAAAGTGTAGACTTCTGGAGTGATA
ATCTGGTGAACAAATATTCTCTGTAGCTGTAAGCAAGTCACTTAATCTTCTACCTCTT
TTCTATCTGCCAAATTGAGATAATGATACTTAACCAGTTAGAAGAGGTAGTGTGAATATTAA
TTAGTTTATATTACTCTTATTGTTGAACATGAACATGCTATGCTAGTGTCTTATTGCT
CAGCTGGCTGAGACACTGAAGAAGTCAGTGAACAAAACCTACACACGTACCTTCATGTGATT
CACTGCCTCCTCTCTACCAGTCTATTCCACTGAACAAAACCTACACACATACCTTCAT
GTGGTTCACTGCCTCCTCTCTACCAGTCTATTCCACTGAACAAAACCTACGACACATAC
CTTCATGTGGCTCAGTGCCTCCTCTCTACCAGTCTATTCCACTGCTGTTGAGCAAGG
GACATGTTGTCGCTGTTCCATTAAACACTGCTCTTACCTTCCAGTCTGTACAGAATG
CTATTCACTGAGCAAGATGATGTAATGGAAAGGGTGTGGCACTGGTGTCTGGAGACCTG
GATTGAGTCTGGTGTATCAATCACCGTCTGTGTTGAGCAAGGATTTGGCTGTTGAA
GCTTATTGCTTCATCTGTAAGCGGTGGTTGTAATTCTGATCTTCCCACCTCACAGTGATG
TTGTGGGATCCAGTGAGATAGAATACATGTAAGTGTGGTTGTAATTAAAAAGTGTAT
ACTAAGGAAAGAATTGAGGAATTAACTGCATACGTTGGTGTGCTTTCAAATGTTGA
AAATAAAAAAAATGTTAAG

FIGURE 98

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185
><subunit 1 of 1, 211 aa, 1 stop
><MW: 22744, pI: 8.51, NX(S/T): 1
MANAGLQLLGFI LAFLGWIGAIVSTALPQWRIYSYAGDNIVTAQAMYEGLWMSCVSQSTGQI
QCKVFDSSLNLSSTLQATRALMVGILLGVIAIFVATVGMKCMKCLEDDEVQKMRMAVIGGA
IFLLAGLAILVATAWYGNRIVQE FYDPMTPVNARYEFGQALFTGWAAASLCLLGGALLCCSC
PRKTTSYPTPRYPKPAPSSGKDYV
```

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-102, 118-142 and 161-187

N-glycosylation site.

amino acids 72-75

PMP-22 / EMP / MP20 family proteins

amino acids 70-111

ABC-2 type transport system integral membrane protein

amino acids 119-133

FIGURE 99

TTCTGGCCAAACCCGGGCTNCAGCTGTTGGCTTCATCTCGCCTCCTGGATGGATCGGC
GCCATCNTCACACTGCCCTCCCCAGTGGAGGATTTACTCCCTATGCTGGCGACAACATCG
TGACCGCCCAGCCCATGTACGAGGGCTGTGGATGTCCNGCGTGTGCAAGGCACCGGGCAG
ATCCAGTGCAAAGTCTTGACTCCTGCTGAATCTGAGCAGCACATTGCAAGCAACCCGTGC
CTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTGTCATGGCCACCGTTGGCATGA
AGTGTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCAATTGGGGGC
GCGATATTCTTCTTGCAAGGTCTGGCTATTTAGTTGCCACAGCATGGTATGGCAATAGAAN
CNTTCAACANTTCTATGACCCATGACCCAGTCAATGCCAGGTACGAATTGGTCA
GGCTCTCTTCACTGGCTGGCTGCTGCTCTCTGCCTCTGGGAGGTGCCCTACTTGT
GTTCCCTGTCCC

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FIGURE 100

ACCCCTGACCAACGCGGCCCCCGACCGNTTCATGGCAAACGCGGNCTCCAGCTGTTGG
GCTTCATTCTCCCCTTCCTGGGATGGACCGGCCATCNTCAGCACTGCCCTGCCAGTG
GAGGATTTACTCCTATNCCGGCNACAACATCGTACCGCCCAGGCCNTGTACGAGGGGCTGT
GGATGTCCTGCGTGTGCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTGACTCCCTGCT
GAATCTGAGCAGCACATTGCAAGCAACCCGTGCCTGATGGTGGTTGGCATCCTCCTGGGAG
TGATAGCAATCTNNNTGCCACCGTTGTNNNTGAAGTGTATGAAGTGCTTGGAAAGACGATGA
GGTGCAGAAGATGAGGATGGCTGTCATTGGGGCGCGATATTCTTCTTGCAGGTCTGGCTA
TTTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCGA

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FIGURE 101

GGGCCGACCATTATCCAACCAGGGNTCACTGTTGGCTCATCTCCCTCCTGGATGAANCAGCGC
CATCNCAGACTCCCTGCCCATGGAGATTNNNCCTATGCTGGCGACAAACATCNTGACCCCC
AGCCATGTACGAGGGCTTGAAACGTCNGCGTGTGCAGANCACCGGGCAGATCCAGTGCAA
AGTCTTGACTCCTGCTGAATCTGNGCAGCACATTGCAGCAACCCNTGCCCTGATGGTGGT
TGGCATTCCCTGGGAGTGATAGCAATCTTGTGGCCACCGTTGGCATGAAGTGTATGAAGT
GCTTGGAAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGCGCGATATTCTT
CTTGCAGGTCTGGCTATTNNNNTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAAT
TCTATGACCCTATGACCCAGTCAATGCCAGGTACGAATTGGTCAGGCTCTTCACTGGC
TGGGCTGCTGCTCTCTGCCTTCTGGGAGGTGCCCTACTTGCTGTTCTGCAG

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FIGURE 102

ATTCTCCCTCCTGGATGGATCGCNCCACCGTCACATTGCCTCCCCANTGGAGGATTNAC
TCCTATGCTGGCGACAACATCGTGACCCCCCAGGCCATTACCGAGGGGCTTGGATGTCNT
GCNTGTCGAGAGCACCAGGCAGATCCCAGTGCAAAGTCTTGACTCCTGCTGAATCTGAG
CAGCACATTGCAAGCAACCGTGCCTTGATGGGTTGGCATCCTCCTGGAGTGATAGCAAC
CTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGAAGACGATGAGGTGCCAGAAG
ATGAGGATGGCTGTATTGGGGCGCATATTCTTGTGCAGGTCTGGCTATTTAGTNGC
CACAGCATGGTATGGCAATAGANTNNTCNNNGNNNTCTATGACCCCTATGACCCCAGTCAATG
CCAGGTACGAATTGGTCAGGCTCTCTTCACTGGCTGGCTGCTGCTCTCTGCCTCTG
GGAGGTGCCCTACTTGCTGTTCTGTCCC

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FIGURE 103

AGAGCACCGGCAGATCCCAGTNCAAAGTCTTGACCTTGCTGAATCTGAGCAGCACATTNC
AAGCAACCCCTGCCTGAAGGTGGTTGNCATCCCCCTGGGAGTGAATAGCAATCTTGTG
GCCACCGTTGGCATGAAGTNTATGAAGTGCTTGAAGACGATGAGGTGCAGAAGATGAGGAT
GGCTGTCATTGGGGCGCGATATTCTTGCAGGTCTGGCTATTTAGTNCCACAGCAT
GGTATGGCAATAGNATNNTCGNGGNTTCTATGACCCATGACCCAGTCAATGCCAGGTAC
GAATTGGTCAGGCTCTTCACTGGCTGGCTGCTGCTCTGCCTCTGGGAGGTGC
CCTACTTGCTGTTCTGTCCCCGAA

FIGURE 104

AGCAATGCCCTGCCCTGCCCCAGTGGAGGATTAATTCTATGNTGGGACAACATTGTGACNGCC
AGGCCATGTACGGGGGGCTGTGGATGTCTCGCTGCGAGAGCACCGGGCAGATCCAGTGC
AAAGTNTTGACTCCTGCTGAATTGAGCAGCACATTGCAAGCAACCCGTGCCTGATGGT
GGTTGGCATCTCCTGGAGTGATAGCAATCTTGTGCCACCGTGGNAATGAAGTGTATGA
AGTGCTTGGAAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGCGCGATATT
CTTNTTGCAGGTCTGGCTATTTAGTTGCCACAGCATGGTATGCAATAGAATNGTTCAAGA
ATTTTATGACCCCTATGACCCCAGTCAATGCCAGGTACGAATTGGTCAGGCTTNTTCACTG
GCTGGGCTGCTGCTTNTTCTGCCCTNTGGGAGGTGCCCTANTTGCTGTTCTGCGAACCC

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FIGURE 105

TCATAGGGGGCGCGATATTTTCTTGCAGGTNTGGTTATTTAGTTGCCACAGCATGGTA
TGGCAATAGAATCGTTCAAGAATTNTATGACCCATGACCCAGTCAATGCCAGGTACGAAT
TTGGTCAGGCTCTNTTCACTGGNTGGGCTGCTGCTTCTNTNNGCCTNTGGGAGGTGCCCTA
CTTTGCTGTTCTG

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30
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10
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FIGURE 106

TTCCCTGGATGGATCCGCCCCATCNTCACATGCCCTGCCCNNTGGAGATTTACNCCTATGC
TGGCGAACAAACATCNTGACCGCCCAGGCCATGTACGAGGGGCTGTGGAATGTCCTGCGTGTC
CCAGAGCACCAGGGCAGATCCAGTGCAAAGTCTTGACTCCTGCTGAATCTGAGCAGCACAT
TGCAAGCAACCNTGCCTTGATGGTGGTGGCATCCTCCTGGAGTGATAGCAATTTGTGG
CCACCGTTGGCATGAAAGTGTATGAAGTGCTTGGAAAGACGATGAGGTGCAGAAGATGAGGAT
GGCTGTCATTGGGGCGCGATATTCTTCTGCAGGTCTGGCTATTTAGNNGCCACAGCAT
GGTATGGCAATCAGACCCNNTCANAAACTCTATGACCTATGACCCAGTCAATGCCAGGTA
CGAATTGGTCAGGCTCTCTTCACTGGCTGGCTGCTGCTTCTCTGCCTCTGGGAGGTG
CCCTACTTTGCTGTTCTGTCCCCGAAAAACAAACCTCTACCCACG

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FIGURE 107

CGGGGCTGCAGCTGTTGGCTTCATCTCGCTTCTGGATGGAATCGGCCATCGTCAGCA
CTGCCCTGCCCATGGAGGATTTACTCNTATGCTGGCACAACATCGTACCNCCCAGGCCA
TGTACGAGGGCTGTGGATGTCNGCGTGCAGAGCACCGGGCAGATCCAGTGCAAAGTCT
TTGACTCCTGCTGAATCTGAGCAGCACATTGCAAGCAACCNTGCCTGATGGTGGTGGCA
TCCTCCTGGGAGTGATAGCAATCTTGTGCCACCGTTGGCATGAAGTGTATGAAGTGCTTG
GAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGCGCGATATTCTTGC
AGGTCTGGCTATTNTAGTTGCCACAGCATGGTATGGCAATAGAATCGTCAAGAATTCTAT
GACCCTATGACCCCAGTCAATGCCAGGTACGAATTGGTCAGGCTCTTCACTGGCTGGC
TGCTGCTTCTCTGCCTCTGGGAGGTGCCCTACTTGTGTTCCCTGCGAA

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FIGURE 108

GCCTGCCGTCAGCTCGCCGGGCACCGCGGCCCTGCCCTCGCCCTCCGCCCTGCGCCTGCAC
CGCTAGACCGACCCCCCCTCCAGCGGCCACCCGGTAGAGGACCCCCGCCGTGCCCG
ACCGTCCCCGCCCTTTGTAAAACCTAAAGCGGGCGCAGCATTACGCTCCGCCCGGT
GACCTCTCAGGGTCTCCCCGCAAAGGTGCTCGCCGCTAAGGAACATGGCGAAGGTGGAG
CAGGTCTGAGCCTCGAGCGCAGCACGAGCTCAAATTCCGAGGTCCCTCACCGATGTTGT
CACCAACCTAAAGCTGGCAACCCGACAGACCGAAATGTGTGTTAAGGTGAAGACTA
CAGCACCAACGCTAGGTACTGTGTGAGGCCAACAGCGGAATCATCGATGCAGGGCCTCAATT
AATGTATCTGTGATGTTACAGCCTTCGATTATGATCCCAATGAGAAAAGTAAACACAAGTT
TATGGTCAGTCTATGTTGCTCCAAGTACACTTCAGATATGGAAGCAGTATGGAAGGGAGG
CAAAACCGGAAGACCTATGGATTCAAAACTTAGATGTGTTGAATTGCCAGCAGAGAAT
GATAAACCACATGATGTAGAAATAAAATTATATCCACAACACTGCATCAAAGACAGAAC
ACCAATAGTGTCTAAGTCTGTAGTTCTTGGATGACACCGAAGTTAAGAAGGTTATGG
AAGAATGTAAGAGGCTGCAAGGTGAAGTTCAGAGGCTACGGGAGGGAGAACAGCAGTTCAAG
GAAGAAGATGGACTGCGGATGAGGAAGACAGTGCAGAGCAACAGCCCCATTTCAGCATTAGC
CCCAACTGGGAAGGAAGAAGGCCCTAGCACCCGGCTTGGCTCTGGTGGTTGTTCTTTA
TCGTTGGTGTATTATTGGGAAGATTGCCCTGTAGAGGTAGCATGCACAGGATGGTAAATTG
GATTGGTGGATCCACCATATCATGGATTAAATTATCATAACCATGTGTTAAAGAAATT
AATGTATGATGACATCTCACAGGTCTGCCCTTAAATTACCCCTCCCTGCACACACATACAC
AGATAACACACACAAATATAATGTAACGATCTTTAGAAAGTTAAAATGTATAGTAACG
ATTGAGGGGGAAAAGAATGATCTTATTAAATGACAAGGGAAACCATGAGTAATGCCACAAT
GGCATATTGTAATGTCATTAAACATTGGTAGGCCTGGTACATGATGCTGGATTACCTC
TCTTAAATGACACCCCTCCTCGCCTGTTGGTGTGGCCCTGGGAGCTGGAGGCCAGCAT
GCTGGGAGTGCAGCTCCACACAGTAGTGTCCCCACGTGGCCACTCCGGCCAGGCTG
CTTCCGTGTCTCAGTTCTGTCCAAGCCATCAGCTCCTGGGACTGATGAAACAGAGTCAGA
AGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTG
TGACTGATTGACCCAGCGCTTGGAAATAATGGCAGTGCTTGTCACTTAAAGGGACCAA
GCTAAATTGTATTGGTCATGAGTCAGTCAAACGTATTCAAGAGATGTTAATGCATA
TTTAACTTATTAAATGTATTTCATCTCATGTTCTTATTGTACAAAGAGTACAGTTAATGC
TGCCTGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTGTGGGCTCCTCT
GTCTCTGGAGAGTCTGGTCATGTTGGAGGTGGGTTATTGGGATGCTGGAGAACAGAGCTGCCA
GGAAGTGTGTTCTGGGTCAAGTAAATAACAACGTACAGGGAGGGAAATTCTCAGTAGTG
ACAGTCACACTAGGTTACCTTTAAATGAAGAGTAGTCAGTCAGTCTCTAGATTGTTCTTATA
CCACCTCTCAACCATTACTCACACTCCAGCGCCAGGTCCAAGTCTGAGCCTGACCTCCCC
TTGGGGACCTAGCCTGGAGTCAGGACAAATGGATCAGGGCTGCAGAGGGTTAGAACAGGAGGGC
ACCAGCAGTTGTGGGTGGGAGCAAGGGAAAGAGAGAAACTCTTCAGCGAATCCTCTAGTAC
TAGTTGAGAGTTGACTGTGAATTAAATTATGCCATAAAAGACCAACCCAGTTCTGTTGA
CTATGTAGCATCTTGAAAAGAAAAATTATAATAAGCCCCAAAATTAAAGAAAA

FIGURE 109

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977
<subunit 1 of 1, 243 aa, 1 stop
<MW: 27228, pI: 7.43, NX(S/T): 2
MAKVEQVLSLEPQHELKFRGPFTDVTTNLKLGNSPTDRNVCFKVKTAPRRYCVRPNSGIID
AGASINVSVMLQPFDYDPNEKSKHKFMVQSMFAPTDTSMDMEAVWKEAKPEDLMDSKLRCVFE
LPAENDKPHDVEINKIISTTASKTETPIVSKSLSSSLDDTEVKVMEECKRLQGEVQRLREE
NKQFKEEDGLRMRKTVQSNSPISALAPTGKEEGLSTRLLALVVLFIVGVIIGKIAL
```

Important features:

Transmembrane domain:

amino acids 224-239

N-glycosylation site.

amino acids 68-71

N-myristoylation site.

amino acids 59-64, 64-69 and 235-240

FIGURE 110

GTCAGTCTCTAGATTGTCCTTATCCCACCTTCACCANTACTCACATTCNAGCGCCCAG
GTCCANGTCTGAGCCTGACTTCCCCTGGGGACCTAGCCTGGAGTCAGGACAATGGNTCGGG
CTGCAGAGGNTTAGAAGCGAGGGCACCAGCAGTTGGTGGGGAGCAAGGGNNGAGAGAAA
CTCTTCAGCGAATCCTCTAGTACTAGTTGAGAGTTGACTGTGAATTAATTTATGCCATA
AAAGACNAACCCAGTTCTGTTGACTATGTAGCATCTGAAAAGAAAAATTATAATAAGCC
CCAAAATTAAGAATTCTTGTCACTTGCTCATGGGGAAATTATTATT
ATCATTATTATTTGCCATTGGAAGGTTAACTTAAAATGAGC

FIGURE 111

TATTGTAAAGGCCATTTAAACCATTGGTAGGCCTTGGTACATGATGCTGGATTACCTCCTT
AAATGACACCNTCCTCGCCTGTTGGTCTGGCCNTGGGGAGCTGGAGCCCCAGCATGCTG
GGGAGTGCAGTCAGCTCCACACAGTAGTCCCCACGTGGCCACTCCGGCCAGGCTGCTTT
CCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTGGACTGATGAACAGAGTCAGAAGCC
CAAAGGAATTGCCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCCTGTTGA
CTGATTGACCCAGCGCTTGGAAATAATGGCAGTGCTTGTTCACTAAAGGGACCAAGCT
AAATTGTATTGGTCATGTAGTGAAGTCAAACGTATTCAAGAGATGTTAATGCATATTAA
ACTTATTAAATGTATTCATCTCATGTTTCTTATTGTCACAAGAGTACAGTTAATGCTGCG
TGCTGCTGAACCTGTGGGTGAACGTGATTGCTGCTGGAGGGCTG

FIGURE 112

CCCTGGTGGTTTGTCTTAATCGTTGGTGTATTNTGGGAAGATTGCTTAGAGGTA
GNATGCACCNGGCTGGTAAATTGGATTGGTGGATCCACCATATCCATGGGATTAAATTAT
CATAACCATGTGTAAAAAGAAATTAATGTATGATGACATNTCACAGGTATTGCCTTAAATT
ACCCATCCCTGNANACACATACACAGATACACANANACAAATNTAATGTAACGATNTTTAG
AAAGTTAAAATGTATAGTAAC

FIGURE 113

GGTGGCCCATTCCCGGCCAGGCTGCTTCCGGTNTTCAGTTCTGTCCAAGCCATCAGCTCC
TTGGGACTGATGAACAGAGTCAGAAGCCAAAGGAATTGCAGTGTGGCAGCATNAGACGTAC
TTGTNATAAGTGAGAGGCCTGTGTTGACTGATTGACCCAGCGCTTGGAAATAATGGCAGT
GCTTTGTTCANTTAAAGGGACCAAGCTAAATTGTATTGGTTATGTAGTGAAGTCAAACCTG
TTATTCAAGAGATGTTAATGCATATTTAANTTAAATTGTATTNTCATGTTTCTTA
TTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAANTNTGTTGGGTGAACGGTATTGC
TGCTGGAGGGCTGTGGGCTCCTCTGTCTTGGAGAGTCTGGTCATGTGGAGGTGGG

FIGURE 114

TGCTTCCGTCTCAGTTCTGTCCAAGCCATCAGCTCCTGGGACTTGATGAACAGAGTC
AGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTG
TGTTGACTGATTGACCCAGCGCTTGGAAATAATGGCAGTGCTTGTTCACTTAAAGGGAC
CAAGCTAAATTGTATTGGTTCATGTAGTGAAGTCAAACTGTTATTAGAGATGTTAATGC
ATATTAACTTATTAAATGTATTCATCTCATGTTTCTTATTGTCACAAGAGTACAGTTAA
TGCTGCGTGC

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FIGURE 115

AAACCTTAAAAGTTGAGGGAAAAGAATGATCCTTATTAATGACAAGGGAAACCNTGN
GATGCCACAATGGCATATTGTAATGTCATTTAACATTGGTAGGCCTGGTACATGATGC
TGGATTACCTCTCTTAAATGACACCCTCCTGCCCTGTTGGTGCTGCCCTGGGAGCTN
GAGCCCAGCATGCTGGGAGTGCGGTCTGCTCCACACAGTAGTCCCCANGGCCANTCCC
GGCCCAGGCTGCTTCCGTGTCTCAGTTCTGTCCAAGCCATCAGCTCCTGGGANTGATGA
ACAGAGTCAGAAGCCAAAGGAATTGCANTGTGGCAGCATCAGANGTANTNGTCATAAGTGA
GAGGCCTGTGTTGANTGATTGACCCAGCGCTTGGAAATAATGGCAGTGCTTGTCANTT
AAAGGGNCCAAGNTAAATTGTATTGGTCATGTAGTGAAGTCAAANTGTTATTGTCACAAGGGT
TTAATGCATATTAANTTATTAATGTATTCATNTCATGTTCTTATTGTCACAAGGGT
ACAGTTAATGCTGCGTGTGAANTCTGTTGGGTGAANTGGTATTGCTG

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FIGURE 116

GGCCCTGGGAGCTGGAGCCCAGCATGCTGGGAGTCGGTCAGCTCACACAGTAGTCCC
CACGTGGCCCACCTCCGGCCCAGGCTGCTTCCGTGTCTCAGTTCTGTCCAAGCCATCAGC
TCCTTGGACTGATGAACAGAGTCAGAACGCCAAAGGAATTGCAGTGGCAGCATCAGACG
TACTCGTCATAAGTGAGAGGCCTGTGTTGACTGATTGACCCAGCGCTTGAAATAATGGC
AGTGCTTGTTCACTTAAAGGGACCAAGCTAAATTGTATTGGTCATGTAGTGAAGTCAAA
CTGTTATTCAAGAGATGTTAATGCATATTAACTTATTAAATGTATTCATCTCATGTTTC
TTATTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAACCTGTTGGGTGAACGGTAT
TGCTGCTGGAGGGCTGTGGGCTCTCTGTCTGGAGAGTCTGGTCATGTGGAGGTGGG

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FIGURE 117

GCAGCTCCGGGTGCTGTGGCCGGCCTGGCGGGCGGCCTCCGGCTCAGGCTGGCTGAGA
GGCTCCCAGCTGCAGCGTCCCCGCCCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGCC
CTCGGGACAAAACAAGCTGGCAGGGTCTCACTTGTGCCCAGGCTGGAGTCAGTGCCA
TGATCATGGTTACTGCAGCCTGACCTCTGGTTCAAGCGATCTGCTGAGTAGCTGGGA
CTACAGGACAAAATTAGAAGATCAAATGGAAAATATGCTGCTTGGTTGATATTTTCA
CCTGGGTGGACCCTCATTGATGGATCTGAAATGGAATGGGATTTATGTGGCACTTGAGAAA
GGTACCCCGGATTGTCACTGAAAGGACTTCCATCTCACAGCCCCGCAATTGAGGCAGATG
CTAAGATGATGGTAAATACAGTGTGCGATCGAATGCCAGAAAGAAACTCCAACTCCCAGC
CTTCTGAATTGGAGGATTATCTTCCTATGAGACTGTTGAGAATGGCACCCGAACCTT
AACCAAGGTGAAAGTTCAAGATTGGTTCTTGAGCCGACTCAAATATCACCACAAAGGGAG
TATCTGTTAGGAGAAAGAGACAGGTGTATGGCACCGACAGCAGGTTCAGCATTGGACAAA
AGGTTCTAACCAATTCCCTTCAGCACAGCTGTGAAGCTTCACGGGCTGTAGTGGCAT
TCTCATTTCCCTCAGCATGTTCTAACTGCTGCCACTGTGTTCATGATGGAAAGGACTATG
TCAAAGGGAGTAAAAGCTAACGGTAGGGTTGAAGATGAGGAATAAAGTGGAGGCAAG
AAACGTCGAGGTTCTAACAGAGGAGCAGGAGAGAACAGTAGTGGTGGTGACCAAAGAGAGGGTAC
CAGAGAGCATCTGCAGGAGAGCGAACGGTGGGAGAAGAAGAAAAAAATCTGGCCGGGTC
AGAGGATTGCCAACGGGAGGCCTTCCTTCAGTGGACCCGGCTAACAGAACCCACATTCCG
AAGGGCTGGGACGAGGAGGCATGGGGACGCTACCTGGACTATGACTATGCTCTGG
GCTGAAGCGTGTCTCACAAAAGAAATACATGGAACCTGGAATCAGGCCAACGATCAAGAAA
TGCCTGGTGGAAATGATCCACTTCTCAGGATTGATAACGATAGGGCTGATCAGTTGGTCTAT
CGGTTTGCACTGTCGACGAATCCAATGATCTCCTTACCAATACTGCGATGCTGAGTC
GGGCTCCACCGGTTGGGGCTATCTGCGTCTGAAAGATCCAGACAAAAAGAATTGGAAGC
GCAAAATCATTGCGGTCTACTCAGGGCACCAAGTGGATGTCACGGGTTCAGAAGGAC
TACAACGTTGCTGTTGCATCACTCCCCCTAAAATACGCCAGATTGCGCTCTGGATTACGG
GAACGATGCCATTGCTTACGGCTAACAGAGACCTGAAACAGGGCGGTGTATCATCTAAA
TCACAGAGAAAACCAGCTGCTTACCGTAGTGAGATCACTCATAGGTTATGCCTGGACTT
GAACCTGTCAATAGCATTCAACATTTCAAAATCAGGAGATTTCGTCACATTAAAAAA
TGTATAGGTGAGATATTGAAACTAGGTGGCACTTCATGCCAGTATGAAATTGATCTTCTT
CATGGTGTGAGTTCTTGTAGAAAAATTGGCTTCTTAAAATTAGACACACTTT
AAACCTCAACAGGTATTATAAACATGTGACTCCTTAATGACTTATTCTCAGGGTCC
TACTCTAACAGAATCTAACAGGATGCTGGTTGTATTAAATGTGAAATTGATAGATAAA
GGTAGATGGTAAAGCAATTAGTATCAGAATAGAGACAGAAAGTTACAACACAGTTGACTA
CTCTGAGATGGATCCATTCACTGCTCATGCCCTCAATGTTATATTGTGTTATCTGTTGGGTCT
GGGACATTAGTTAGTTTTGAAGAATTACAATCAGAAGAAAAGCAAGCATTATAAA
CAAAACTAACAACTGTTACTGCTTAAAGAAATAACAATTACAATGTGTATTATTAAAAAA
TGGGAGAAATAGTTGTTCTATGAAATAAACCTAGTTAGAAATAGGAAAGCTGAGACATT
TAAGATCTCAAGTTTATTAACTAACATACTCAAATATGGACTTTCATGTATGCATAGGG
AAGACACTTCACAAATTATGAATGATCATGTGTGAAAGCCACATTATTTATGCTATACAT
TCTATGTATGAGGTGCTACATTAGGACAAAGAATTCTGTAATCTTCAAGAAAGAGT
CTTTTCTCCTGACAAATCCAGTTGTATGAGGACTATAGGGTGAATTCTCTGATTAG
TAATTAGATATGCTCTTCAAAATGAATAAAATTATGAATATGA

FIGURE 118

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253
<subunit 1 of 1, 413 aa, 1 stop
<MW: 47070, pI: 9.92, NX(S/T): 3
MENMLLWLIFFTPGWTLIDGSEMEWDFMWHLRKVPRIVSERTFHLSPLAFADAKMMVNTVC
GIECQKELPTPSLSELEDYLSYETVFENGTRTLTRVKVQDLVLEPTQNITTKGVSVRRKRQV
YGTDSRFSILDKRLFNTFPFSTAVKLSTGCSGILISPQHVLAAHCVHDGKDYVKGSKKLRV
GLLKMRNKSGGKKRRGSKRSRREASGGDQREGTREHLQERAKGRRKKSGRGQRIAEGRPS
FQWTRVKNTHIPKGWARGGMGATLDYDYALLELKRAHKKKYMELGISPTIKKMPGGMIHFS
GFDNDRADQLVYRFCVSDESNDLLYQYCDAESGSTGSGVYRLKLDPDKNWKRKIIAVYSG
HQWVDVHGVQKDYNVAVRITPLKYAQICLWIHGNDANCAYG
```

Important features:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 90-93, 110-113 and 193-196

Glycosaminoglycan attachment site.

amino acids 236-239

Serine proteases, trypsin family, histidine active site.

amino acids 165-170

FIGURE 119

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTAGCACCACTACTGGAT
GTGACAGCAGGCAGAGGGAGCACTTAGCAGCTTATTCACTGTCGATTCTGATTCCGGCAAGG
ATCCAAGC**ATG**GAATGCTGCCGTGGCAACTCCTGGCACACTGCTCCTCTTCTGGCTTC
CTGCTCCTGAGTTCCAGGACCGCACGCTCCGAGGGAGGACGGACGGCTATGGATGCCTG
GGGCCATGGAGTGAATGCTCACGCACCTGCAGGGAGGGCCTCCTACTCTGAGGCCT
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC
TGCCCACCAGAACAGGTGATTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA
CCATGGCCAGTTTATGAATGGCTTCTGTCTAATGACCCGTACAACCCATGTTCACTCA
AGTGCCAAGCCAAAGGAACAAACCTGGTGTGAACTAGCACCTAACGGCTTAGATGGTACG
CGTTGCTATACAGAACATCTTGGATATGTGCATCAGTGGTTATGCCAAATTGTTGGCTGCGA
TCACCAAGCTGGGAAGCACCGTCAAGGAAGATAACTGTGGGTCTGCAACGGAGATGGTCCA
CCTGCCGGCTGGTCCGAGGGCAGTATAAATCCCAGCTCTCGCAACCAATGGATGATACT
GTGGTTGCACCTCCCTATGGAAGTAGACATATTGCCTGTCTTAAAGGTCTGATCAGTCACTT
ATATCTGAAACCAAAACCCCTCCAGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAA
CTTCCCTGTGGACAATTCTAGTGTGGACTTCCAGAAATTCCAGACAAAGAGATACTGAGA
ATGGCTGGACCACTCACAGCAGATTTCATTGTCAAGATTGTAACCTGGCTCCGTGACAG
TACAGTCCAGTTCATCTTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTCTTTC
CTTGCTCAGCAACCTGTGGAGGAGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGG
AGCAACCGTGTGGTGTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC
CAAGCTTCAGGAGTGCAACTTGGATCCTGTCCAGCCAGTGACGGATAACAAGCAGATCATGC
CTTATGACCTCTACCATCCCCTCCTCGGTGGAGGCCACCCATGGACCGCGTGCTCCTCC
TCGTGTGGGGGGGCATCCAGAGCCGGCAGTTCTGTGTGGAGGAGGACATCCAGGGCA
TGTCACTTCAGTGGAAAGAGTGGAAATGCATGTACACCCCTAAGATGCCATCGCGAGCCCT
GCAACATTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCGTGACAGTGACATGT
GGCCAGGGCCTCAGATAACCGTGTGGCCTCTGCATCGACCATCGAGGAATGCACACAGGAGG
CTGTAGCCAAAAACAAAGCCCCACATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATA
AACCCAAAGAGAAACTCCAGTCAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA
GAAGAAGGAGCTGCTGTCAAGAGGAGCCCTCG**TAA**GGTAAAGCACAGACTGTTCTATA
TTTGAAACTGTTTGTAAAGAAAGCAGTGTCACTGGTTGTAGCTTCATGGTTCTGA
ACTAAGTGTAAATCATCTCACCAAAGCTTTGGCTCTCAAATTAAAGATTGATTAGTTCAA
AAAAAAA

FIGURE 120

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847
<subunit 1 of 1, 525 aa, 1 stop
<MW: 58416, pI: 6.62, NX(S/T): 1
MECCRATPGTLLLFLAFLSSRTARSEEDRDGLWDAWPWSECSRTCGGGASYSLRRCLS
SKSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNDPDNPCSLKCQ
AKGTTLVVELAPVKLDGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCR
LVRGQYKSQLSATKSDDTVVALPYGSRHIRLVLKGPDHLYLETKTLQGTKGENSLSTGTFL
VDNSSVDFQKFPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFFPCS
ATCGGGYQLTSAECYDLRSNRVVADQYCHYYPPENIKPKPKLQECNLDPASPASDGYKQIMPYD
LYHPLPRWEATPWTACSSSCGGGIQSRAVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNI
FDCPKWLAQEWSPECTVTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPK
EKLPVEAKLPWFQQAQELEEGAAVSEEPS
```

Important features:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 251-254

Thrombospondin 1

amino acids 385-399

von Willebrand factor type C domain proteins

amino acids 385-399, 445-459 and 42-56

FIGURE 121

CGGACGCGTGGCGGCGCTGCGGAACCTCCGTGGAGGGCCGGTGGCCCTCGGCCTGAC
AGATGGCAGTGGCACTGCGGCGGAGTACTGGCGCTCTGGCGGGCGCTGTGGCTGGCG
GCCCGCCGGTCTGGGGCCAGGGTCCAGCGGCTGCGCAGAGGCGGGACCCGGCCTCAT
GCACGGGAAGACTGTGCTGATCACCGGGCGAACAGCGGCCTGGCCGCCACGGCCGCCG
AGCTACTGCGCCTGGAGCGCGGGTGATCATGGCTGCCGGACCGCGCGCGCCAGGGAG
CGGGCGGGTCAGCTCCGCCGAGCTCCGCCAGGCCGCGAGTGCAGGCCAGAGCCTGGCGT
CAGCGGGTGGCGAGCTCATAGTCCGGAGCTGGACCTCGCCTCGCTGCCTCGGTGCGCG
CCTTCTGCCAGGAAATGCTCCAGGAAGAGCCTAGGCTGGATGTCTGATCAATAACGCAGGG
ATCTCCAGTGCCCTACATGAAGACTGAAGATGGTTGAGATGCAGTTGGAGTGAACCA
TCTGGGCACTTCTACTCACCAATCTCTCCTGGACTCCTCAAAAGTTAGCTCCCAGCA
GGATTGTGGTAGTTCTTCCAAACTTATAAAACGGAGACATCAATTGATGACTTGAAC
AGTGAACAAAGCTATAATAAAAGCTTTGTTAGCCGGAGCAAACGGCTAACATTCTTT
TACCAAGGAACTAGCCCGCCGCTTAGAAGGCACAAATGTCACCGTCAATGTGTTGCATCCTG
GTATTGTACGGACAAATCTGGGAGGCACATACACATTCCACTGTTGGTCAAACCACTCTC
AATTTGGTGTATGGCTTTTCAAAACTCCAGTAGAAGGTGCCAGACTCCATTATT
GGCCTCTTCACCTGAGGTAGAAGGAGTGTCAAGGAAGATACTTGGGATTGTAAAGAGGAAG
AACTGTTGCCAAAGCTATGGATGAATCTGTTGCAAGAAAACGGATATCAGTGAAGTG
ATGGTTGGCCTGCTAAAATAGGAACAAAGGAGTAAAGAGCTGTTATAAAACTGCATATCAG
TTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTACTTGAAGAAAAGAATTG
ATATTGGAATAGCCTGCTAAGAGGTACATGTGGTATTGGAGTTACTGAAAAATTATT
TGGGATAAGAGAATTTCAGCAAAGATGTTAAATATATAGTAAGTATAATGAATAATAA
GTACAATGAAAAATACAATTATATTGAAACTGGCAAGCATGGATGACATATTA
ATATTGTCAAGATTAAAGTGACTCAAAGTGCTATCGAGAGGTTTCAAGTATCTTGAGTT
TCATGCCAAAGTGTAACTAGTTACTACAATGTTGGTGTGGAAATTATCTGC
CTGGTGTGACACAAGTCTTACTTGAATAATTACTGGTAC

FIGURE 122

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747
<subunit 1 of 1, 336 aa, 1 stop
<MW: 36865, pI: 9.15, NX(S/T): 2
MAVATAAAVLAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAE
LLRLGARVIMGCRDRARAEEAAGQLRRELQAAECGPEPGVSGVGELIVRELDLASLRSVRA
FCQEMLQEEPRLDVLINNAGIFQCPYMKTEDGFEMQFGVNHLGHFLLTNLLLGLLKSSAPSR
IVVVSSKLYKYGDINFDDLNSEQSYNKSFCYSRSKLANILFTRELARRLEGTNVTVNVLHPG
IVRTNLGRHIHIPLLVKPLFNLVSWAFFKTPVEGAQTSIYLIASSPEVEGVSGRYFGDCKEEE
LLPKAMDESVARKLWDISEVMVGLLK
```

Important features:

Signal peptide:

amino acids 1-21

Short-chain alcohol dehydrogenase family protein

amino acids 134-144, 44-56 and 239-248

N-glycosylation site.

amino acids 212-215 and 239-242

FIGURE 123

GGGGATTGTAAAGAGGAAGNACTGTGCCAAAGNTATGGATGAATCTGTTGCAAGAAAATTN
TGGGATATCAGTGAAGTGATGGTTNGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTT
TATAAAACTGCATATCAGTTATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTACT
TGAAGAAAAAGAATTGATATTGGAATAGCCTGNTAAGAGGNACATGTGGGTATTTGGAG
TTACTGAAAATTATTTGGGATAAGAGAATTTCAGCAAAGATGTTAAATATATAGT
AAGTATAATGAATAATAAGTACAATGAAAATACAATTATATTGAAAATTATAACTGGC
AGCATGGATGACATATTAATATTGTCAGAATTAAAGTGAUTCAAAGTGCTATCGAGAGGTT
TTCAAGTATCTTGAGTTCATGCCAAAGTGTAACTAGTTACTACAATGTTGGTGT
TGTGTGGAAATTATCTGCCTGGCTT

FIGURE 124

GAGAGGACGAGGTGCCGCTGCCCTGGAGAATCCTCCGCTGCCGTGGCTCCGGAGCCCAGCC
CTTTCTAACCCAACCCAACCTAGCCCAGTCCCAGCCGCCAGCGCCTGTCCTGTACGGAC
CCCAGCGTTACC**ATG**CATCCTGCCGTCTCCTATCCTAACCGACCTCAGATGCTCCCTCT
GCTCCTGGTAACCTGGGTTTTACTCCTGTAACAACGTGAAATAACAAGTCTTGCTACAGAGA
ATATAGATGAAATTTAAACAATGCTGATGTTGCTTAGTAAATTTATGCTGACTGGTGT
CGTTTCAGTCAGATGTTGCATCCAATTTGAGGAAGCTCCGATGTCATTAAGGAAGAATT
TCCAAATGAAAATCAAGTAGTGTGCTTGCAGAGTTGATTGTGATCAGCACTCTGACATAGCCC
AGAGATAACAGGATAAGCAAATACCCAAACCCCAAATTGTTGTAATGGGATGATGATGAAG
AGAGAATAACAGGGGTAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAAG
TGACCCCATTCAAGAAATTGGGACTTAGCAGAAATCACCCTTGATCGCAGCAAAGAA
ATATCATTGGATATTTGAGCAAAGGACTCGGACAACTAGAGTTTGAAACGAGTAGCG
AATATTTGCATGATGACTGTCCTTCTTCATTTGGGATGTTCAAAACCGGAAAG
ATATAGTGGCGACAACATAATCTACAAACCACCAGGGCATTCTGCTCCGGATATGGTGTACT
TGGGAGCTATGACAAATTTGATGTGACTTACAATTGGATTCAAGATAATGTGTTCTCTT
GTCCGAGAAATAACATTTGAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTCTCAT
ACTCTTCACATGAAAGAAGATACAGAAAGTTAGAAATATTCCAGAATGAAGTAGCTCGGC
AATTAATAAGTAAAAAGGTACAATAACTTTACATGCCGATTGTGACAAATTAGACAT
CCTCTTCTGCACATACAGAAAACCTCCAGCAGATTGTCCTGTAATCGCTATTGACAGCTTAG
GCATATGTATGTGTTGGAGACTTCAAAGATGTATTAATTCCATCATGGACCTGACCCAAGT
TATTTGACTTACATTCTGGAAAACGTGCACAGAGAATTCCATCATGGACCTGACCCAAGT
ACAGCCCCAGGGAGAGCAAGCCAAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTCCAGAA
ACTAGCACCCAGTGAATATAGGTATACTCTATTGAGGGATCGAGATGAGCTT**AAAAACTTG**
AAAAACAGTTGTAAGCCTTCAACAGCAGCATCACCTACGTGGTGGAAATAGTAAACCTA
TATTTCTATAATTCTATGTGTATTTTATTTGAATAAACAGAAAGAAATTAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 125

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57689
<subunit 1 of 1, 406 aa, 1 stop
<MW: 46927, pI: 5.21, NX(S/T): 0
MHPAVFLSLPDLRCSLLLLTVWVFTPVTTEITSLATENIDEILNNADVALVNFYADWCRFSQ
MLHPIFEEASDVIKEEFPNENQVVFARVDCDQHSDIAQRYRISKYPTLKLFRNGMMMKREYR
GQRSVKALADYIRQQKSDPIQEIRDLAETTLDRSKRNIIGYFEQKDSDNYRVFERVANILH
DDCAFLSAFGDVS KPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNWIQDKCVPLVREI
TFENGEELT EEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLH
IQKTPADCPVIAIDSFRHMYVFGDFKDVLIPGKLKQFVFDLHSGKLHREFHHGPDPDTAPG
EQAQDVASSPPESSFQKLAPSEYRYTLLRDRDEL
```

Important features:

Signal peptide:

amino acids 1-29

Endoplasmic reticulum targeting sequence.

amino acids 403-406

Tyrosine kinase phosphorylation site.

amino acids 203-211

Thioredoxin family proteins

amino acids 50-66

FIGURE 126

ATTAAGGAAGAATTCCAATGAAAATCAAGTAGTNTTGCCAGAGTNGATTGTGATCAGCA
CTCTGACATAGCCCAGAGATAAGCAAATACCCAACCCCTCAAATTGTTCGTAATG
GGATGATGATGAAGAGAGAATAAGGGGTCAAGCGATCAGTGAAAGCATTGGCAGATTA

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FIGURE 127

AGAGGCCTCTGGAAAGTTGTCGGGTGTCGCCGCNGGAGCCGGTCGAGAGGACNAGG
TGCGCTGCCTGGAGAACCTCCGCTGCCGTCGGCTCCGGAGCCAGCCCTTCCTAACCC
AACCCAACCTAGCCCNGTCCCAGCCGCAGCGCCTGTCCTGTCNCGGANCCCAGCGTNACC
ATGCATCCTGCCGTCTCCTATCCTAACCGACCTCAGATGCTCCCTCTGCTCCTGGTAAC
TTGGGTTTTACTCCTGTAACAACGTAAATAACNNGTCTGATACNNAGAATATAGATGAAA
TTTAAACNATGCTGATGTGGCTTAGTCATTGACTGGTGTGTTAGTCAG
ATGTGGCATCCAATTGGAGGANGCTTCCGATGTCATTAGGAAGAATTCCAATGAAA
TCAAGTAGTGTGTTGCCAGAGTTGATTGATCAGCACTCTGACATAGCCCAGAGATACAGGA
TAAGCAAATACCCAACCCCTCAAATTGTTGTAATGGGATGATGAAGAGAGAATACAGG
GGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGC

FIGURE 128

GCCCACGCGTCCGATGGCGTTCACGTTCGCGGCCCTCTGCTACATGCTGGCGCTGCTGCTCA
CTGCCCGCCTCATCTTCTTGCACATTGGCACATTATAGCATTGATGAGCTGAAGACTGAT
TACAAGAATCCTATAGACCAGTGTAAATACCCCTGAATCCCCTGTACTCCAGAGTACCTCAT
CCACGCTTCTTGTGCATGTTCTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATA
TGCCCCTTGGCATATCATATTGGAGGTATATGAGTAGACCAGTGTAGAGTGGCCAGGA
CTCTATGACCTACAACCACATGAATGCAGATATTCTAGCATATTGTAGAAGGAAGGATG
GTGCAAATTAGCTTTATCTTCTAGCATTTCACCTATATGGCATGATCTATGTT
TGGTGAGCTCTTAGAACAACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAGCCAC
CAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGT
TACTTTAAAAAATGACTCCTTATTTTAAATGTTCCACATTTGCTTGTGAAAGACTG
TTTCATATGTTACTCAGATAAAGATTAAATGGTATTACGTATAAATTAATATAAAAT
GATTACCTCTGGTGTGACAGGTTGAACTTGCACTTCTTAAGGAACAGCCATAATCCTCTG
AATGATGCATTAATTACTGACTGTCTAGTACATTGGAAGCTTTGTTATAGGAACCTGTA
GGGCTCATTGGTTCATGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGC
TTCTGATGAAGTGAAGGAAATTGTATATCTGACTAGTGGAAACTTCATGGTTCCCTCATCTGTC
ATGTCGATGATTATATATGGATACATTACAAAAATAAAAGCGGAAATTTCCTCGCTT
GAATATTATCCCTGTATATTGCATGAATGAGAGATTCCATATTCCATCAGAGTAATAAA
TATACTTGCTTAATTCTAACGATAAGTAAACATGATATAAAATATGCTGAATTACTT
GTGAAGAATGCATTAAAGCTATTAAATGTGTTTATTGTAAGACATTACTTATTAAG
AAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTGCAGG
TACTACAGATTTCAAAACGTGAATGAGAGAAAATTGTATAACCACCTGCTGTTCTTAGT
GCAATACAATAAAACTCTGAAATTAAGACTC

FIGURE 129

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330
<subunit 1 of 1, 144 aa, 1 stop
<MW: 16699, pI: 5.60, NX(S/T): 0
MAFTFAAFCYMLALLTAALIFFAIWHIIAFDELKTDYKNPIDQCNLNPVLPEYLIHAF
CVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLA
FYLLAFFYYLYGMIYVLVSS
```

Important features:

Signal peptide:

amino acids 1-20

Type II transmembrane domain:

amino acids 11-31

Other transmembrane domain:

amino acids 57-77 and 123-143

FIGURE 130

ATTATAGCATTGATGAGCTGAAGACTGATTACAAGATCCTATAGACCAGTGTAAATACCCCTG
AATCCCCTGTACTCCCAGAGTACCTCATCCACGCTTCTGTGTATGTTCTTGTGC
AGCAGAGTGGCTTACACTGGGTCTCAATATGCCCTCTGGCATATCATATTGGAGGTATA
TGAGTAGACCAGTGATGAGTGGCCCAGGACTCTATGACCCCTACAACCACATGAATGCAGAT
ATTCTAGCATATTGTCAGAAGGAAGGATGGTGCAAATTAGCTTTATCTCTAGCATTTT
TTACTACCTATATGGCATGATCTATGTTGGTAGCTCTAGAACACACAGAAGAATT
GGTCCAGTTAAGTGCATGCAAAAAGCCACCAATGAAGGGATTCTATCCAGCAAGATCCTGT
CCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTAAAAAATG

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FIGURE 131

CGGACGCGTGGGGAAACCCTCCGAGAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGG
GAACAAGATGGCGGCCGAAGGGAGCCTCTGGGTGAGGACCCAACTGGGCTCCGCCGC
TGCTGCTGCTGACCATGGCCTGGCGAGGTTGGGACCGCTCGGCTGAAGCATTGAC
TCGGTCTTGGGTGATACGGCGTCTGCCACCGGGCCTGTCAGTTGACCTACCCCTGCACAC
CTACCCCTAAGGAAGAGGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTCAATTGTC
AGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACA
GAAGCATATTCCAATCTGATGAGCAATATGCTGCCATCTTGGTGCCAGAATCAGCTGCC
ATTCGCTGAACGTGAGACAAGAACAACTTATGTCCTGATGCCAAAAATGCACCTACTCTTC
CTCTAACTCTGGTGGAGGTGACATGATGGACTCCGCACAGAGCTTCATAACC
TCTTCATGGACTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTCCAGTCTAAGCC
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GCAAAATGTCCTATCTGCAAATGAGAAATTACAAGCGCACAGGAATTTCTTGAAAGATGGA
GAAAGTGTGGCTTTAAGATGCGCTCTCTTAACACTCTGGGTGGATTAACTACAACCTCT
TGTCCCTCTGGTGTGGATTGCTTGGATTGTTGTGCAACTGTTGCTACAGCTGTGGAGC
AGTATGTTCCCTCTGAGAAGCTGAGTATCTATGGTACTGGAGTTATGAATGAACAAAAG
CTAAACAGATATCCAGCTCTCTCTTGTGGTTAGATCTAAACTGAAGATCATGAAGA
AGCAGGGCCTACCTACAAAAGTGAATCTGCTCATTCTGAAATTTAAGCATTTCCTTT
AAAAGACAAGTGTAAAGACATCTAAAATTCCACTCCTCATAGAGCTTTAAAATGGTTCA
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FIGURE 132

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26847
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KEEELYACQRGCRLFSICQFVDDGIDLNRTKLECESACTEAYSQSDEQYACHLGCQNQLPFA
ELRQEQLMSLMPKMHLLFPLTLVRSFWSDMMDSAQSFITSSWTFYLQADDGKIVIFQSKPEI
QYAPHLEQEPTNLRESSLSKMSYLNQMRNSQAHRNFLEDGESDGFLRCLSLNSGWILTTLVL
SVMVLLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVRSKTEDHEEAG
PLPTKVNLAHSEI
```

Important features:

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 241-260

N-glycosylation site.

amino acids 90-93